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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: September 25, 2001, 17:34:53; Search time 20.66 Seconds (without alignments)

Berfect score: 3489

Perfect score: 3489

Sequence: 10S-09-462-845-2

Sequence: 1 MKKLITADDITAIVSVTDPO......HPRQRIKRLNYISSWFDQHL 657

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
	1104 5	31 7	637	-	TC-00-016-080-1	Segment and i
10	635	18.2	622	٠,	US-08-664-646A-2	7 7
m	635	18.2	622	2	US-09-066-285-2	'n
4	635	18.2	622	m	US-09-261-006-2	7
5	635		622	4	US-08-951-088-2	7
9	272	7.8	755	Ŋ	PCT-US93-07923-3	m
7	272	7.8	759	Ŋ	PCT-US93-07923-2	2,
80	272	7.8	166	Н	US-08-230-491A-3	3,
6	272	7.8	166		US-08-619-280A-3	Sequence 3, Appli
10	272	7.8	166	7	US-08-940-391-3	3,
11	257.5	7.4	760	Н	US-08-230-491A-2	2,
12	257.5		760	-	US-08-619-280A-2	7
13	57	7.4	760	7	US-08-940-391-2	7
14	145.5	4.2	593	Ŋ	PCT-US93-07923-11	11,
15	$\overline{}$	4.1	588	Н	US-07-903-466-3	e,
16	141.5	4	588	S	PCT-US93-05794-3	3,
17	129	Э.	305	3	US-08-965-600-1	7,
18	126.5		317	Н	US-07-688-299-1	1,
19		3.6	317		US-07-980-517A-1	Sequence 1, Appli
20	i.		318	Н	US-07-688-299-3	Seguence 3, Appli
21	126.5	•		7	US-07-688-299-13	Sequence 13, Appl
22	115.5			æ	US-08-965-600-3	Q.
23	115	3.3		7	US-08-602-359A-37	
	114.5	•		7	US-08-126-564A-31	31,
25	114.5	3.3	579	2	PCT-US94-09143-31	Sequence 31, Appl
	113.5	3.3	006	7	US-08-813-940-4	Sequence 4, Appli
27	109.5	3.1	528	3	US-08-747-221B-37	37,

Sequence 29, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 64, App]	Sequence 68, App.	Sequence 2, Appl	Patent No. 5268290	Sequence 2, Appl:	Sequence 3, Appl:	3,	Sequence 2, Appl	Sequence 34, Appl	Sequence 2, Appl	Sequence 2, Appl.	Sequence 2, Appli	5,	Sequence 4, Appl	Sequence 2, Appl
US-08-190-802A-29	US-08-883-534-6	US-09-204-764-6	US-08-190-802A-64	US-08-190-802A-68	US-08-308-818-2	5268290-2	US-08-714-402-2	US-08-883-534-3	US-09-204-764-3	US-09-130-242-2	US-08-602-359A-34	US-08-258-188-2	US-08-526-813-2	PCT-US95-08554-2	US-09-139-064-2	US-09-139-064-4	US-09-264-737-2
Н	7	٣	-	7	7	9	7	7	٣	4	7	-	-	2	4	4	3
428	597	597	198	798	798	626	1112	909	909	1088	346	758	758	758	428	428	999
3.1	3.1	3.1	3.1	3.1	3.1	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	2.9	2.9	5.9
108.5	108	108	107	107	107	104.5	104.5	104	104	104	103.5	103.5	103.5	103.5	102.5	102.5	101.5
28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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78 LAFIS-DREGDAAQLYIMSTEGGEARKLIDIPYGVSKPLWSPDGESILVTISLGEGESID 136
                                                                                                                                                                                                             137 DREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAF 196
                                                                                                                                                                                                                                                                                                                                                        127 DDEDFVFDDDVPVWF-----DNMGFFDGEKTTFWVLDTEAEEIIE-----QFEKPRF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 EQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHFIASV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |::: |||| :: | :: | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 GRVNLWLWDGKAERVV-----TGDHWI-------YGLDVSDGKALLLI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 TKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMRPAQM 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 EGETTYPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGD 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 NWISFHGVSDIGYFFTDWQ-----LEHDMFEDTEKLWDRSPLKYAANVETPLLILHGER 598
                                                                               19 DPRIR--GNLIAYILTKANMKDNKYESTVVVEDLETGS----RRFIENASMPRISPDGRK 72
                                       18 DPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWTHGEKRSTDPRWSPDGRT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  599 DDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPDGKW----LVFSANLTETDDASKP-----HDVYIMSLESGDLKQVTPHRGSFGSSSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485 YGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQRSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 PDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTE-MLDVHLADALIGD--SLIGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Murphy et al.
TITLE OF INVENTION: Amidases
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,285
FILING DATE:
CLASSIFICATION:
PRIOR ADDITE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: 3,5 INCH DISKETTE IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/664,646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09066285 Patent No. 5985646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 BECKER FARM ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6 BECALL.
CITY: ROSELAND
STATE: NEW JERSEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                   321 GTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHFIA--SVTKPDRPSELYSIPL 378
                                                                                                                          GQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHG 438
                                                                                                                                                                  FTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMG 618
                                                              300 ATDGPRANLFRVNLDGKIERVIGGDRSVESFDIG-DYIAFTAQDAVT----PTELYIYRD 354
                                                                                                                                                                                                                                                        GPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVD 498
                                                                                                                                                                                                                                                                                                                                                                                     EAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQRSISNWISFHGVSDIGYF 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query.Match 18.2%; Score 635; DB 2; I Best Local Similarity 29.4%; Pred. No. 1.6e-48; Matches 194; Conservative 113; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619 KETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Murphy et al.
TITLE OF INVENTION: Amidases
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
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NAME: Challes J. Herron
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 331400-53
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08664646A Patent No. 5877001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       622 AMINO ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: June 17, CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: PROTEIN US-08-664-646A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM MEDIUM TYPE: 3.5 INC
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US-08-664-646A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                              472
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ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD

NEW JERSEY

ZIP: 07068

ROSELAND USA

STREET: CITY: R COUNTRY: STATE:

Amidases

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

TITLE OF INVENTION:

OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/261,006

FILING DATE:

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2

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27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAFIS-DREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDGESILVTISLGEGESID 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPDGKW----LVFSANLTETDDASKP-----HDVYIMSLESGDLKQVTPHRGSFGSSSFS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 EQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHFIASV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : |:||| || ||| || : || || || || EEKA--PVIVFVHGGFKGMYGHREVYEMQLMASKGYYVVFVNPRGSDGYSEDFALRVLER 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NWISFHGVSDIGYFFTDWQ-----LEHDMFEDTEKLWDRSPLKYAANVETPLLILHGER 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 LAFTCFNEEKKETEIWVADIQTLSAKKVLSTK-NVRSMQWNDDSRRLLVV----GFKRR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDEDFVFDDDVPVWF-----QFEKPRFDGEKTTFWVLDTEAEEIIE-----QFEKPRF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTE-MLDVHLADALIGD--SLIGGA 304
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                                                                                                                                                                                                                                                                                                                                                                                                               18.2%; Score 635; DB 2; 29.4%; Pred. No. 1.6e-48;
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                                                                                            331400-53
                                          NAME: Charles J. Herron
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 3314C
TELEPOMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FILING DATE: June 17, 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            LENGTH: 622 AMINO ACIDS TYPE: AMINO ACID STRANDEDNESS:
                                                                                                                                                                                                                                                                                             TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN
US-09-066-285-2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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78 LAFIS-DREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDGESILVTISLGEGESID 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 194; Conservative 113; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.2%; Score 635; DB 3;
Best Local Similarity 29.4%; Pred. No. 1.6e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 GRVNLWLWDGKAERVV-----TGDHWI------
                                                                                                                                            331400-53
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664,646
FILING DATE: June 17, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                            28,019
                                                                                                                                        REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                     NAME: Charles J. Herron
REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                622 AMINO ACIDS
                                                                                                                                                                                                      TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 AMINO ACID
                                                                                                                                                                                                    201-994-1744
                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: PROTEIN US-09-261-006-2
                                                                                                                                                                                                                                                                                   AMINO ACID
                                                                                                                                                                                                                                                                                                                        LINEAR
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Sequence 2, Application US/09261006 Patent No. 6004796 GENERAL INFORMATION:

US-09-261-006-2

APPLICANT: Murphy et al.

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375 EEKA--PVIVFVHGGPKGMYGHRFVYEMQLMASKGYYVVFVNPRGSDGYSEDFALRVLER 432
                                                             485 YGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQRSIS 544
                                                                                                                                                                               545 NWISFHGVSDIGYFFTDWQ-----LEHDMFEDTEKLWDRSPLKYAANVETPLLILHGER 598
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                                                                                                                                                                                                                                                                                                                                  18 DPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWTHGEKRSTDPRWSPDGRT 77
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Best Local Similarity 29.4%; Pred. No. 1.6e-48;
Matches 194; Conservative 113; Mismatches 260; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Murphy et al.
TITLE OF INVENTION: Amidases
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
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CLASSIFICATION: 435
RIGOR APPLICATION 1047A:
APPLICATION NUMBER: 08/664,646
FILING DATE: June 17, 1996
ATORNEY/AGENT INCRMATION:
NAME: Charles J. Herron
REGISTRATION NUMBER: 28,019
REFERENCE/COCKET NUMBER: 331400-
TELECOMMUNICATION INFORMATION:
TELEPRANCE 201-994-1740
TELEPANCE: 201-994-1740
TELEPANCE: 201-994-1740
TELEPANCE: 201-994-1740
TELEPANCE: 201-994-1740
TELEPANCE: 201-994-1700
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APPLICATION NUMBER: US/08/951,088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08951088 Patent No. 6136583 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: MS-DOS
WORD PERFECT 5.1
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STREET: 6 DLL
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINEAR
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ZIP: 07068
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US-08-951-088-2
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282 GRVNLWLWDGKAERVV-----TGDHWI-------YGLDVSDGKALLLI 317
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                                                                      SPDGKW----LVFSANLTETDDASKP----HDVYIMSLESGDLKQVTPHRGSFGSSSFS 247
                                                                                                                                                                       248 PDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTE-MLDVHLADALIGD--SLIGGA 304
                                                                                                                                                                                                                                                                           305 EQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHFIASV 364
                                                                                                                                                                                                                                                                                                                                                                          365 TKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMRPAQM 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 EGETTYPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGD 484
                                                                                                                   174 S-SGLWHGDAIVVNVPHRE---GSKPALFKFYDIVLW--KDGEEEKLF-ERVSF--EAVD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   599 DDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 SDGKRILLRGKKK--KRRISEHDWLY-LWDGELKPIYEGPLDVWEAKLTEGKVYFLTPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Morimoto, Chikao
APPLICANT: Schlossman, Stuart F.
APPLICANT: Tanaka, Toshiaki
TITLE OF INVENTION: HUMAN CD26 AND METHODS FOR USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 0210-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
PCT/US93/07923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 00530/055002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application PC/TUS9307923 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934,162
FILING DATE: 21-A0G-1992
APPLICATION NUMBER: 07/832,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 225 Franklin Street CITY: Boston STATE: Macon
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REGISTRATION NUMBER: 34,819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        566 HDMFEDTEKLWDRSPLKYAAN--VETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKL 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 LPTPEDNLDHYRNSTVMSRAENFKQVEYLLIHGTADDNVHFQQSAQISKALVDVGVDFQA 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 YRHICYFQIDKKDCTFITKGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYT 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 -SVTNATSIQIT-----APASMLIGDHYLC-----DVTWATQERISLQWLRRIQNYSV 313
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                                                                                                                                                                                                                                                                                                       90 SINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWV---- 144
                                                                                                                                                                                                                                                                                                                                                                                  145 ----TWSPVGHKLAYVWNND----IYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEE 195
                                                                                                                                                                                                                                                                                                                                                                                                                      ---GVSKPLWSPDGESILVTISLGEGESIDDRE--KTEQDSYEPVEVQGLSYKRDGKGLT 164
                                                                                                                                                                                                                                                                15 SVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIY-----ETKTGGSVPWTHGEKR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 LDKMLQNVQMPSKKLDFIILNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVF
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                                                                                                                                                                                                                            Matches 153; Conservative 113; Mismatches 285; Indels 200;
                                                                                                                                                                                          DB 5; Length 755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 VFSAYSALWWSPNGTFLAYA-----QFNDTEVPLIEYSFYSDESLQ--
                                                                                                                                                                                                                                                                                                                                             66 STDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLT----DIPY-
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                                                                                                                                                                                          7.8%; Score 272; DB 5 20.4%; Pred. No. 9e-16;
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GENERAL INFORMATION:
APPLICANT: MorImoto, Chikao
APPLICANT: Schlossman, Stuart F.
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                Best Local Similarity
                                                                            amino acid
                                                                                                                 ; TOPOLOGY: linear
PCT-US93-07923-3
                                                                                             STRANDEDNESS:
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                                                          LENGTH:
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241 ---YPKTVRVPYPKAG------ 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 ----TWSPVGHKLAYVWNND-----IYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEE 199
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APPLICANT: Tanaka, Toshiaki
TTTLE OF INVENTYON: HUMAN CD26 AND METHODS FOR USE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                COUMTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDUIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.8%; Score 272; DB 5; 20.4%; Pred. No. 9.1e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/055002
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
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1-19930819
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PRIOR APPLICATION NUMBER: 07/934,162
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: 07/832,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/832,211
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                    E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                              Massachusetts
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                                                                                                         ADDRESSEE:
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COUNTRY:
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                                                                    400 IPEEIQYATE-----DGVMVNG---W--LMRPAQMEGETTYPLILNIHGGPHMMYGHTYF 449
                                                                                                                                                                       612 VDNKRIAIWGWSYGGYVTSMVLGSGSGVFKCGIAVAPVSRWEYYDSV-----YTERYMG 665
     --TGANDKFVR--EHTIS 399
                                   434 KVTCLSCELNPER-CQYYSVSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSA 492
                                                                                                                                                                                                                        507 IDPKRLGVTGGSYGGFMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLE 565
                                                                                                                                                                                                                                                                                                   566 HDMFEDTEKLWDRSPLKYAAN--VETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKL 623
                                                                                                                                                                                                                                                                                                                        | | : | : | : | : | : | 66 LPTPEDNLDHYRNSTVMSRABNFKQVEYLLIHGTADDNVHFQQSAQISKALVDVGVDFQA 725
                                                                                                    493 LDKMLQNVQMPSKKLDFIILNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADIVF
                                                                                                                                               H---EFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rettig, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Garin-Chesa, Pilar; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR
TITLE OF INVENTION: FIBROBLAST ACTIVATION PROTEIN 'AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 7.8%; Score 272; DB 1; Length 766; Best Local Similarity 20.4%; Pred. No. 9.3e-16; Matches 153; Conservative 113; Mismatches 285; Indels 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE 3.5 inch 1.2 MB STORAGE
                                                                                                                                                                                                                                                                                                                                                                           624 VRFPNASHNL-SRTGHPRQRIKRLNYISSWF 653
                                                                                                                                                                                                                                                                                                                                                                                                                 726 MWYTDEDHGIASSTAHQHIYTHMSHFIKQCF 756
------PDRPSELYSIPLGQEEK--QL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/230,491A
FILING DATE: 20-APRIL-1994
CLASSIFICATION: 435
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STREET: 805 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hanson, No. 5587299man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1UD 330
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 848-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 766 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT - ASC II
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08230491A
Patent No. 5587299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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US-08-230-491A-3
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15 SVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIY-----ETKTGGSVPWTHGEKR 65

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101 SINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWV---- 155
                                                                                                              ----TWSPVGHKLAYVWNND-----IYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEE 206
                                                                                                                                                                   110 ---GVSKPLWSPDGESILVTISLGEGESIDDRE--KTEQDSYEPVEVQGLSYKRDGKGLT 164
                                                                                                                                                                                                                                                                                 RGAYAQLVLVSV-KSGEMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----YDIEQGRLTCLTEMLDVHLADALIGDSLIGG-AEQRPIWTKDSQGFY-VIGTDQG 325
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APPLICANT: Rettig, Wolfgang, Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
TITLE OF INVENTION: ALPIA, AND USES THEREOF
NUMBER OF SOUGHOES: 10
ADDRESSEE: Felfe & Lynch
                                                       66 STDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLT-----DIPY------
                                                                                                                                                                                                                                                                                                                                                                                             224 MSLESGDLKQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNAT---LSKAWL-----
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TT: 805 Third Avenue
New York City
T: New York
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COMPUTER: IBM PS/2
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624 VRFPNASHNL-SRTGHPRQRIKRLNYISSWF 653

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Matches 153; Conservative 113; Mismatches 285; Indels 200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.8%; Score 272; DB 1; Length 766; 20.4%; Pred. No. 9.3e-16;
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                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5330.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                   APPLICATION NUMBER: US/08/619,280A
FILING DATE: 18-MARCH-1996
                                                                                                                                                                                                       NAME: Hanson, No. 5767242man D. REGISTRATION NUMBER: 30,946
                                                                                                                           APPLICATION NUMBER: 08/230,491 FILING DATE: 20-APRIL-1994 ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                     PRIOR APPLICATION DATA:
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                                                                        CLASSIFICATION:
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                                                                                                                                                                               APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd U.A.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION
TITLE OF INVENTION: PROTEIN ALPHA, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 STDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLT----DIPY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 20.4%; Pred. No. 9.36
Matches 153; Conservative 113; Mismatches
733 MWYTDEDHGIASSTAHQHIYTHMSHFIKQCF 763
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01-0CT-1997
N: 530
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/619,280 FILING DATE: 18-MARCH-1996 APPLICATION NUMBER: 08/230,491
                                                                                                  US-08-940-391-3
; Sequence 3, Application US/08940391
; Patent No. 5965373
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               SEE: Felfe & Lynch
: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS
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                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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: USA
                                                                                                                                                               GENERAL INFORMATION:
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amino acid

; TOPOLOGY: US-08-230-491A-2

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500 LDKMLQNVQMPSKKLDFIILNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVF 559
|: : |:| : |:| 278 -SVTNATSIQIT-----APASMLIGDHYLC-----DVTWATQERISLQWLRIQNYSV 324
                                                                                                        325 MDICDYDESSGRWNCLVARQHIEMSTT----GWVGRFRPSEPHFTLDGNSFYKIISNEEG 380
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                                                             273 ----YDIEQGRLTCLTEMLDVHLADALIGDSLIGG-AEQRPIWTKDSQGFY-VIGTDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08230491A
Patent No. 5587299
GENERAL INFORMATION:
APPLICANT: Rettig, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Garin-Chesa, Pilar; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TITLE OF INVENTION: FIBROBLAST ACTIVATION PROTEIN 'AND USES
                                                                                                                                                       STGIYYISIE--GLVYPIRLEKEYINSFSLSPDEQHFIASVTK---
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/230,491A
FILING DATE: 20-APRIL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, No. 5587299man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 330
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 638-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                805 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUD 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: FELFE & LYNCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PS/2
OPERATING SYSTEM: I
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                                                                                                                                                                                                                                                                                             152 QGLSYKRDGK---GLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPA-----FSPDGKWL 203
                                                                                                                                                                                                                                                                                                                                           186 NG----PTKYALWWSPNGKFL 221
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                                                                                                41 SYTSNIWIYETKIGGSVP----WIHGEKRSTDPRWSPDGRTLAFISD-----REGDAAQL 91
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Patent No. 5767242
GENERAL INFORMATION:
APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
ITLE OF INVENTION: ALPHA, AND USES THEREOF
NUMBER OF SEQUENCES: 10
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APPLICATION NUMBER: US/08/940,391
FILING DATE: 01-0CT-1997
CAGSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/619,280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/290,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-940-391-2
Sequence 2, Application US/08940391
; Patent No. 5965373
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APPLICATION NUMBER: 08/230
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: BOS Third Avenue CITY: New York City
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
US-08-940-391-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
7.4%; Score 257.5; DB 1; Length 760;
Best Local Similarity 21.2%; Pred. No. 1.8e-14;
Matches 154; Conservative 119; Mismatches 272; Indels 181; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 SYTSNIWIYETKTGGSVP----WTHGEKRSTDPRWSPDGRTLAFISD-----REGDAAQL 91
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                                                                                                                                storage
                                                                                                                                Diskette, 3.5 inch, 2.0 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 RLEKEYINSFSLSPDE-----
                                                                                                                                                                                                                                                                                                                                                      NAME: Hanson, No. 5767242man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5330.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,280A
FILING DATE: 18-MARCH-1996
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRL-1994
ATTORNEY/AGENT INFORMATION:
              : 805 Third Avenue
New York City
New York
Felfe & Lynch
                                                                                                                                                                    OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
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                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                    COMPUTER: IBM PS/2
                                                                                                                                                                                                                                              FILING DATE: 18 CLASSIFICATION:
                                                                        USA
                                                                                        10022
ADDRESSEE:
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                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 YIMSTEGGEARKLTDIPYGVSKPLWSPDGESILVTISLGEGESIDDREKTEQDSYEPVEV 151
                                                                                                                                                                                                                                                                                            Indels 181; Gaps
                                                    566 GMVIALVDGRGTAFQGDKLLYAVYRKLGVYEVEDQITAVRKFIEMG-FIDEKRIAIWGWS 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 SYTSNIWIYETKTGGSVP----WTHGEKRSTDPRWSPDGRTLAFISD-----REGDAAQL 91
                                                                                                                                                                     459 GYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGS
                                                                                                                      519 YGGFMTNW-IVGQTNRFKAAVTQRSISNWISFHGVSD---IGYFFTDWQLEHDMFEDTEK
                                                                                                                                                                                                                                                    575 LWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FLBROBLAST ACTIVATION
TITLE OF INVENTION: PROTEIN ALPHA, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 21.2%; Pred. No. 1.8e-14;
Matches 154; Conservative 119; Mismatches 272;
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131 YIYDLSNGEFVRGNELPRPIQYLCWSPVGSKLAYVYQ----NNIYLKQRPGDPPFQ-ITF 185
                                      152 QGLSYKRDGK----GLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPA-----FSPDGKWL 203
                                                                                                                                                      222 AY-AEFNDKDIPVIAYSYYGDEQYPRTINIPYPKAGAKNPVV------RIFIIDTTYP 272
                                                                           186 NG----RENKIFNGIPDWYYEEEML-------PTKYALWWSPNGKFL 221
                                                                                                                  204 VFSANLTETD------DASKPHDVYIMSLESGDLKQVTPHRGSFGSSSFSPDGRYL 253
                                                                                                                                                                                                                        296 -----IGDSLIGGA----EQRPIWTKDSQGFYVIGTDQ-GSTGIYYI--SIEGLVYPI 341
                                                                                                                                                                                                                                                                                                 342 RIEKEYINSFSLSPDE-----QHF 360
                                                                                                                                                                                                                                                                                                                                                                                       392 SGKWEAINIFRVIQDSLFYSSNEFEEYPGRRNIYRISIGSYPPSKKCVTCHLRKERCQYY 451
                                                                                                                                                                                                                                                                                                                                                                                                                                361 IASVTK------PDRP-SELY-----SIPLGQEEKQLTGANDKFVREHTISIP- 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 TASFSDYAKYYALVCYGPGIPISTLHDGRTDQBİKİLEENKELENA-----LKNİQLPK 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYF--HEFQVLAAK- 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||: | : : :: | | : |||:|| EBIKKLEVDEITLWYKMILPPQFDRSKKYPLLIQVYGGPCSQSVRSVFAVWISYLASKE 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 YGGFMTNW-IVGQTNRFKAAVTQRSISNWISFHGVSD---IGYFFTDWQLEHDMFEDTEK 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             575 LWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLS 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 ALLGNEKEYKNATLSK-----AWLYDIEQGRLTCLTEMLDVHLADAL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application PC/TUS9307923
GENERAL INFORMATION:
APPLICANT: Morimoto, Chikao
APPLICANT: Schlossman, Stuart F.
APPLICANT: Tanaka, Toshiaki
TITLE OF INVENTION: HUMAN CD26 AND METHODS FOR USE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55sx
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US93/07923 FILING DATE: 19930819 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Dis
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STATE: Massac
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PCT-US93-07923-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 MDICDYDESSGRWNCLVARQHIEMSTT----GWVGRFRPSEPHFTLDGNSFYKIISNEEG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 STGIYYISIE--GLVYPIRLEKEYINSFSLSPDEQHFIASVTK------- 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 YRHICYFQIDKKDCTFITKGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GVSKPLWSPDGESILVTISLGEGESIDDRE--KTEQDSYEPVEVQGLSYKRDGKGLT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 -SVTNATSIQIT-----APASMLIGDHYLC-----DVTWATQERISLQWLRRIQNYSV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----YDIEQGRLTCLTEMLDVHLADALIGDSLIGG-AEQRPIWTKDSQGFY-VIGTDQG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 KVTCLSCELNPER-CQYXSVSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSA 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 -------PDRPSELYSIPLGQEEK--QL-------TGANDKFVR--EHTIS 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 SVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIY-----ETKTGGSVPWTHGEKR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 MSLESGDLKQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNAT---LSKAWL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.2%; Score 145.5; DB 5; Length 593;
Best Local Similarity 19.7%; Pred. No. 0.00014;
Matches 113; Conservative 75; Mismatches 197; Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 STDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLT-----DIPY----
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                                                                                                                                                     00530/055002
                                 FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
07/934,162
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Patent No. 5395767
                                                                                                                              34,819
                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Murnane, John P.
APPLICANT: Painter, Robert B.
                    FILING DATE: 21-AUG-1992
APPLICATION NUMBER: 07/8
                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                      NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
PCT-US93-07923-11
                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                     593
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                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 EKWQKEKDRIKSFTTNEKAILEQNFRDLVRDLEKQKEEVRAALEQREQDAVDQVKVIMDA 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 GFYVIGTDQGSTGIYY----ISIEGLV 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 TKTGGSVPWTHGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 VSKPLWSPDGESILVTISLGEG------ESIDDREKT--EQDSYEPVE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 -----AEGKSLGSALKPGEGRSALFAGNEWRRPIIQFVESGDDKNSNYFSMDSME--- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 VQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKWLVFSANLT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ------GR---RSPYAGLQL-----GAAKKPPVTFAEKGDVRKS------133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 ETDDASKPHDVYIMSLESGDLKQVTPHRGSFGSSSFSPDGRYLAL----LGN-EKEYKNA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
4.1%; Score 141.5; DB 1; Length 588;
Best Local Similarity 19.3%; Pred. No. 0.00032;
Matches 138; Conservative 75; Mismatches 212; Indels 291; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Steuart Street Tower, 18th Fl., One Market STREET: Plaza
                  APPLICANT: Yu, Loh C.
TITLE OF INVENTION: Gene for Ataxia-Telangiectasia
TITLE OF INVENTION: Complmentation Group D (ATDC)
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 91-077-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9275
TELEFAX: 415-543-4219
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/903,466 FILING DATE: 19920622
                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                 ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               588 amino acids
                                                                                                                                                                                                                       RY: San Francisco 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
APPLICANT: Kapp, Leon N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                    NUMBER OF SEQUENCES: 4:
                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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09vc19 drosophila
031048 porphyromon
09fg66 arabidopsis
000199 homo sapien
012884 homo sapien
087543 capnocytoph
06523 porphyromon
09hmn5 homo sapien
P70092 xenopus lae
091651 xenopus lae
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09xaj2 streptomyce
09phc9 xylella fas
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019086 caenorhabdi
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09x217 felis silve
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DT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update) HYPOTHETICAL 73.5 KDA PROTEIN PH0863.
NO	PH0863. Dyronogons horikoshii
808	Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN	(1)
RP C	SEQUENCE FROM N.A.
RX.	MEDLINE=98344137; PubMed~9679194;
RA	Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA RA	Yamamoto S., Sekine M., Baba SI., Kosugi H., Hosoyama A., Nagir I., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA	Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA	Aoki KI., Yoshizawa T., Nakamura Y., Kobb F.T., Horikoshi A.,
KA ₽₽	Masuchi I., Shizuya n., Alfachi n., "Complete sequence and gene organization of the genome of a hyper-
RT	thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
RL G	DNA Res. 5:55-76(1998).
7 C	EMBL; APCOUCUS, BAAASSSILI, THEATPING TPRO00134
X X	
SO	SEQUENCE 642 AA; /3491 MW; E9D3D28E92D/34bD CRC04;
Ö	lery Match 31.7%; Score 1104.5; DB 1; Length 642;
mΣ	Best Local Similarity 39.9%; Pred. No. 3.3e-68; Matches 255; Conservative 126; Mismatches 217; Indels 41; Gaps 21;
Qy	27 RAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWTHGEKRSTDPRWSPDGRTLAFISDR 84
Db	35 KAVFQVTEISLKDDDYFSKLYLYDGKRVKPFTSGNKDS-NPRFSPNGKLIAFTSKRDK 91
ΟŸ	85 EGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDGESILVTISLGEGESIDDREKTEQD 144
Db	92 EGKESELYVIPTDGGEARLLAKFKYGINNLRFTEDGKSLAVVTPIDVEKKGND 144

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNV-2000 (TrEMBLrel. 14, Last annotation update)
ACYLANINO-ACID-RELEASING EMZYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE)
(APH) (ACYLAMINOACYL-PEPTIDASE)
                                                                         DVH--IIREIPFWFNGVGWIYGKRNVVYLVDVESGKKKRLTPKNLNVDQIRFH-NGR-LY 200
                                                                                                                                          205 FSANLTETDDASKP--HDVYIMSLESGDLKQVTPHRGSFGSSSFSP--DGRYLALLGNEK 260
                                                                                                                                                                                                                                                                                     261 EYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSLIGGAEQRPIWTKDSQGFYVI 320
145 SYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKWLV 204
                                                                                                                                                                                                     201 FTA---QEDRERKPLISDLYV--LENRKVRKLTP--GKWRILDFLPLDDGSFV-LKANTL 252
                                                                                                                                                                                                                                                                                                                                                                                                                         321 GTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHFIA--SVTKPDRPSELYSIPL 378
                                                                                                                                                                                                                                                                                                                                                       253 ERGIPTNAHIYHYDPKTGELKKLTKDLDRNAYNSLNSD--VRGSQRAELVYKEGWIYYV- 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 ATDGPRANLFRVNLDGKIERVIGGDRSVESFDIG-DYIAFTAQDAVT----PTELYIYRD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-KEKKVIDEN-KWIKGYILSKPEHFKVKASDGVEIDAWVMKPVNFRKGKKYPAILEIHG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVD 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVIQRSISNWISFHGVSDIGYF 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      559 FTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAPDQIGKDPWSNLEGYWEKSPLKYAPNVETPLLIIHSTEDYRCWLPEALQLFISLKYLG 601
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NCBI_TaxID=29292;
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31.4%; Score 1096.5; DB 1; Length 631;
Best Local Similarity 38.2%; Pred. No. 1.1e-67;
Matches 258; Conservative 119; Mismatches 233; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248288; CAB50502.1;
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223 IMSLESGDLKQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTC 282
                                                                                                                                                                                                                                  264 LFKE-DLSAYNSLNSD--VRGAQRAELIFKDG-WIYFVATDGPRANLFRVNLDGKVERVI 319
56 TFGRK-DANPRFSPDGRLIAFTSKRSKEGRESELYLMPVDGGEARLLAKFKYGIKDLRFS 114
                          118 PDGESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRD-------GKGLT 164
                                                          ---ITPVEVKKVANEKEDVHVIDEIPFWFNGIGWI 154
                                                                                                                                                                                                          LTEMLDVHLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIR 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makaroya K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                165 RGAYAQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKP--HDVY
                                                                                                                                                                                                                                                                 343 LEKEYINSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPE
                                                                                                                                                                                                                                                                                              320 RGDRSVESFSVG---DYIAFTAQDATTPTELYALRDG-KEKRITDFN-AWIRDYKLSKPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 EIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAV
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NCBI_TaxID=1299;
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Science 286:1571-1577(1999).
EMBL; AE001879; AAF09754.1; -
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614 VKRLELIVGWFERWL 628
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InterPro; IPR000379; -.
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                                                         115 EDGKEIAV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 EQGRLTCLTEMLDVHLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLVYPIRLEKEY-----INSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 GGV-----KAYDHDPQGVISAFTAN---EHGVALI----RESATRFPEVELNGQRVTDL 390
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                                                                                                             Gaps
                                                                                                                                                                        ----KDSYTSNIWIYETKTGGSV 57
                                                                                                                                                                                                                                                                                                                                                                   130 WSPDGRFIAFT------TTADTED-----KRDERGEARVLTRPVYRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 ENGQHRRLDTGHDHPVGDAVGGDCHVGAFPEGPRWL-DGDTLLFSSTVRGSVGLFTAHIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 NDKF---VREHTISIPEELQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446 HTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              506 HIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HDMFE--DTEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94;
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                                                               Length 655;
                                                           Ouery Match 28.5%; Score 995; DB 2; Length 65
Best Local Similarity 36.0%; Pred. No. 1.3e-60;
Matches 250; Conservative 102; Mismatches 248; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
659Aa LONG HYPOTHETICAL ACYLAMINO-ACID-RELEASING ENZYME.
APE1832.
42CCCBA0FB72F200 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             624 VRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                               DDITAIVSVTDPQYAPDGTRAAYVKSQVNQE----
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72626 MW;
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SEQUENCE
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QYATEDGVMVNGWLMRPAQMEGETT--YPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAV 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 IKWSSOGSMIGYLSRKPTG----REWKPYSERDVLEIDRIPVWFDSEGWVFDRYWGLTV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 HLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYIS----IEGLVYPIRLE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 KEYINSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEI 404
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S. I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Magai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K. I., Kubota K.,
Makamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KKLITADDITAIVSVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWI----YETKTGGS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KKPVTPEDIIRLTFVSNPSVSPEGDKVAYLATKADEKENTYRSGIWLAEEDSYRPLTGG- 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 LKQVTPHRG-SFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTLNTVNSDARGPSCLRGMYW - - DDNGHLYYGVHNAGRMVVMKSRPLGEAEAVLDP - - - S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 659;
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                                                                                                                                                                                                                                                                                                                                                                    659 AA; 73895 MW; 475E78DEE5863551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 27.6%; Score 962.5; DB 1; Best Local Similarity 34.8%; Pred. No. 2.3e-58; Matches 235; Conservative 120; Mismatches 274;
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(TrEMBLrel. 16, Last sequence update)
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                                                                                                                                                                                                                                   crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL, AP000062; BAA0835.1; -.
InterPro; IPR000379; -.
SEQUENCE 659 AA; 73895 MW; 475E7
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EMBL, AE005114; AAG20414-1; P.C., Propression of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of 
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                                                                                                                                                        Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                     YUXL OR VNG2302G.
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                                                                                                                                                                                                                                                                                                                                                                                                       Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankal A., Kosugi H., Hosoyama A., Fukui S., Maqazi Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nomura N., Sako Y., Kikuchi H.; Kubota K., "Complete genome sequence of an aerobic hyper-thermophilic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 AEQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHFIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 --SPTEPPEVYRFKGGDVER-VSSINRWVVEEFRLYKPRRVEVEAE-GEVVEGWYIEP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 TSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSLESGDLKQVTPHRGSFGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 TSE--DLGVLTAEPCGN-SIYYVTLRRWAD---PLDTVVKSVPISGGEPETVLEGLTVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 SFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLT-EMLDVHLADALIGDSLIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 VTKPDRPSELYSIPLGÖEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMRPAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 MEGETTYPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQRSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                              Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248; Indels
                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
572AA LONG HYPOTHETICAL ACYLAMINO-ACID-RELEASING ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62902 MW; 1EEE3752567B9510 CRC64;
                                    651
                   609 RLLKKHGVDTRLVRYPGEGHDLSRSGDPGHVVDRIERIAAWFD
612 IALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 697; DB 1;
Pred. No. 4.4e-40;
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                                                                                                                             572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     crenichaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL; RO000064; BAA61302.1; -.
Interpro; IPR000379; -.
                                                                                                                                                                    Created)
                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99310339; PubMed=10382966;
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33.5%;
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                                                                                                                                                                01-NOV-1999 (TrEMBLrel.
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Best Local Similarity
Matches 199; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572 AA;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=56636;
                                                                                                                                                                                                                                                            Aeropyrum pernix
                                                                                                                                                                                                                                                                                                 Aeropyrum.
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27;
'Pyrococcus abyssi genome sequence: insights into archaeal chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 RGAYAQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKW----LVFSANLTET-DDASKPH 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVYIMSLESGDLKQVTPHRGSFGSSSF---SPDGRYLALLGN-EKEYKNATLSKAWLYDI 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 NIYLW--KDGEEEKL-----FEKVSFHAIDSDGKNILLYGKPEKKYMSEH-DKLYIYD- 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 ETKTGGSVPWTHGEKR----STDPRWSPDGRTLAFIS-DREGDAAQLYIMSTEGGEARKL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 LEAK-NIRSLEWNDDSRRLLV-----IGFKRRDDEDFIFEDDVPAWF---DNMGFF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQGRLTCLTEMLDVHLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLVYPIRLEKEYINSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKFVRE 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 TDIPYGVSKPLWSPDGESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLT 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MMQLIFGDTVMTSIEWNEKTFTKFAYLSDPRIR--GSTIAYVLTKANLDNNKYESTI-VL 57
                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 DGEKTTFWIVDTEAEEVIE-----QFEKPRFS-SGVWHGDSIVVNVPYRDTIPRYFKYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 --GEVKGIMDSIDREAGQAKI-------KDGKVYFTL-YEEGSVNLYL--WD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 AAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVT
                                                       604 IEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRORIKRLNYISSWFDQHL 657
                                                                                           499 IDQALAMHTALKVNGKESFLVVFTKGSHGHSILASPRHRRKRLELKLKWIKEKL 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ48287; CAB50354.1; -.
InterPro; IPR000379; -.
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                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Best Local Similarity 28.4%; Pred. No. 5.7e-38;
Matches 194; Conservative 132; Mismatches 263;
                                                                                                                                                                                          632 AA
                                                                                                                                                                                                                                Created)
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                           Pyrococcus abyssi
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete Sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.",
516 GGSYGGFMTNWIVGQTNRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLEHDMFEDTEKL 575
                      .27 ISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AVGFKREDEDFIFEDDVPAWF---DNMGFFDGEKTTFWVIDTEGEEVIE--- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---QFEKPRFS-SGIWHGDSIVVSV------PHRDVIPRYFKYWDIYLW--KDGEE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 DPRWSPDGRTLAFIS-DREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDGESILVT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DVYIMSLESGDL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 KQVTPHRGSFGSSSF---SPDGRYLALLGN-EKEYKNATLSKAWLYDIEQGRLTCLTEML 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVHLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEY 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 DREVAQAKIRNGKV------YFTLFEEGSVNLYL--WDGEVREIAKGKHW 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 TAIVSVTDPQYAPDGTR---AAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWTHGEKRST 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 TKFAYLSDPR----TRKNLVAYVLTKANLESNKYENTI-VIENLEDGSRKFI----EDAS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=53953;
                                                                               576 WDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSR
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                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.9%; Score 660; DB 1; L ilarity 28.2%; Pred. No. 1.8e-37; Conservative 130; Mismatches 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 HKADHGDPAFSPDGKW----LVFSANLTETDDASKPH----
                                                                                                                                                                                                                                                                                               622 AA
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                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                               593 RGSPRHRMKRYKLFMEFFERKL 614
                                                                                                                                                        636 TGHPRQRIKRLNYISSWFDQHL 657
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                                                                                                                                                                                                                                                                                               PRELIMINARY;
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01-AUG-1998 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
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SEGUENCE 622 AA; 7
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Best Local Similarity
Matches 189; Conserv
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MEDLINI-2003-07; Pubmed-10910347;

SIMPSON A.J.G., Reinach F.C., Arraya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S.,
Buenco M.R.P., Camarco A.A., Camaryo L.E.A., Carraro D.M., Entones M.R.S.,
Buenco M.R.P., Camarco A.A., Camaryo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Coutinho L.L., Cristofani M., Dias Neto E., Docena C., El-Dorry H.,
Facincani A.P., Ferreira A.J.S., Ferreira V.C.A. Ferro J.A.,
Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Rainer M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
Ho P.L., Hoheisel J.D., Junqueira M.L., Kitajima J.P.,
Krieger J.E., Kuramae E.E., Landais M.R., Laite L.C.C.,
Rainer B.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Marques M.V., Martins E.R.C., Palmieri D.A., Paris A.,
Marques M.V., Martins E.R.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Mono D.H., Nagain M.A., Mascimento A.L.F., Nesquero J.B.,
Cousagio R.B., Roberto P.G., Redrigates V., de Rosa A.J.M.,
Changoto R.R., Peretara G.A., Peretara H.A. Jr., Pesquero J.B.,
Changoto R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
Changoto R.B., Roberto P.G., Peretara H.A. Jr., Pesquero J.B.,
Changoto R.B., Roberto P.G., Peretara H.A. Jr., Pesquero J.B.,
Changoto R.B., Roberto P.G., Peretara H.A. Jr., Pesquero J.B.,
Changoto R.B., Roberto P.G., Peretara H.A. Jr., Pesquero J.B.,
Changoto R.B., Roberto P.G., Peretara H.A. Jr., Pesquero J.B.,
Changoto R.B., Roberto P.G., Peretara H.A. Jr., Pesquero J.B.,
Changoto R.B., Roberto P.G., Peretara H.A. Jr., Pesquero J.B.,
Changoto R.B., Roberto P.G., Peretara H.A. Jr., Pesquero J.B.,
Changoto R.B., Peretara G.A., Peretara H.A. Jr., Pesquero J.B.,
Changoto R.B., Peretara M.A., Verjovski-A
                                                                                                                           SID-LELDGWYIKPEIKEGEKA-PVIVFVHGGPKGMYGYYFKYEMQLMASKGYYIVYVNP 415
                                                                                                                                                                                                        RGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWI 527
                                                                                                                                                                                                                                     VGQTNRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLEHDMFEDTEKLWDRSPLKYAANV 587
                                                                                                                                                                                                                                                                                                                                    588 ETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLN 647
348 INSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYA 407
                                            303 IMGFDA---DERLIYLKETATRPAELYL--WDGEERQLTDYNGLIFKKLKTFEPRHFRFK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                        : |||::| | |||::|
535 KAPLLLIHSLEDYRCPLDQSLMFYHVLKDLGKEVYIAIFFKKGAHGHSIRGSPRHRMKRYK 594
                                                                                                    TEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAVVYINP
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                         170 QLVLVSVK------SGEMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDA-S 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 KPHDVYIMSLESGD----LKQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWL 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 DRIVFSAGVFQVCGSDLSCTKRKLDEKKNAKASGVVFEQLFVRHWDTWNDGRRNTL-FIA 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 YDIEQGRLTCLTEMLDVHLADALIGDSLIGGAEQRPIWTK-------DSQGFYVIGTD 323
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                                                                               Gaps
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Query Match 13.6%; Score 473; DB 2; Length 709; Best Local Similarity 22.7%; Pred. No. 2e-24; Matches 163; Conservative 138; Mismatches 288; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bruchhaus I., Hellberg A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF059279; AAF20265.1; -.
                                                                                                                                                      9 DITAIVSVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGS-
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
DIPEPTIDYL-PEPTIDASE (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                   310 APMKIVGNYMHLSTQIEGNVYIVGLDTSKSELFREDVN---IITQKGTAGSFVFTTGII 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641
                                                                                                                                                                                          M-----STEGGEARKLTDIPYGVSK-PLWSPDGE-SILVTISLGEGESIDDREKTEQDS 145
                                                                                                                                                                                                                                     YEPVEVQGLSYKRDGKGLTRGAYAQLV------LVSVKSGEMKELT----SH 187
                                                                                                                                                                                                                                                                                                                                                  253 DNKGYDNQPLFNNDGSLLYYLSMSAPKDESDKSVLKSX---DFKEKIIRDITGKIDLSFS 309
                                                                                                                                                                                                                                                                                                                                                                                                                  YPIRLEKEYINSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTI 398
                                                                                                                                                             Gaps
                                                                                                                                              42 YTSNIWI-YETKTGGSVPWTHGEKRSTDPRWSP-----DGRTLAFISDREGDAAQLYI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHNGQIAKIENDKIIDITSTPISIDTFEMISVDGKLRGLASMTVFPGMTLEESAK-----
                                                                                                                                                                                                                                                                                             236 PHRGSFGSSSFSPDGR---YLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLD----
                                                                                                                                                                                                                                                                                                                                                                         -----VHLADALIGDSLIGGAE-QRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLV
                                                                                                                                                                                                                                                                                                                                                                                                                               SIPEEIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFHEF--QVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKGYAVVY INPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEA IKRDPHIDPKRLGVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     517 GSYGGFMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLEHDMFEDTEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        523 ASYGGYMMNWINSQNTGRFKCIICHDGIMDSEGSYYYMDEMYFL-ETEFGYPMYEDNTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 WDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSR
                                                                                                                                                                                                                                                                                KADHGDPA-----FSPDGKWLVFSANLTETDDASKPHDVYIMSLESG-DLKQVT-
                                                                                                             Best Local Similarity 24.5%; Pred. No. 4e-22;
Matches 167; Conservative 119; Mismatches 270; Indels 126;
                                                                                                     DB 5; Length 663;
                                                                    25EF2B47D0CC36DF CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         665 AA
                                                                                                    12.6%; Score 439; 24.5%; Pred. No. 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Entamoebidae; Entamoeba
                               Pfam; PF00326; Peptidase_S9; 1.
PRIWTS; PR00862; PR0LIGOPTASE.
NON TER
SEQUENCE 663 AA; 76572 MW; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---PYNSIDWHTQVFNWLAKYL 660
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                        IPR002470; -
  IPR000379;
IPR001375;
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01-OCT-2000
InterPro;
                        InterPro;
             InterPro;
                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPDGKWLVFSANLTETDDASKPHDVYIMSLESGDLKQ---VTPHRGSFGSSSFSPDGR-- 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 NVYIVGLDTSKSELTREDVN---IITQKGTAGSFVFTTTGIIY-----EY-NSFTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------PQELF-LYENKVIKQITHINOEVLSTIKFGEYKEIHYTGANNDQIHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -YLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLD------VHLADALIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 YYLSMSAPKDESDKSVLKS---YDFNQKVIRDITGNIDLSFSAPMKVVGNYMHLSTQIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 EQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 WLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFHEF--QVLAAKGYAVVYINPRGSHGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQ-TNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 DAFLKAIRKNWGGWPFEDLMKGMDYLKTSEPLVDIDNACAMGASYGGYMMNWINSQNTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 DSLIGGAE-QRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKAAVTQRSISNWISFHGVSDIGYFFTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLI
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                                                                                                                                                                                                                                                                                                                                                                                                                           59;
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                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                          the EMBL/GenBank/DDBJ databases
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
591AA LONG HYPOTHETICAL ACYLAMINO-ACID-RELEASING ENZYME
                                                                                                                                                                                                                                                                                                 76529 MW; D5D71BD45D42AA94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       12.4%; Score 433.5; DB 5; 27.7%; Pred. No. 9.7e-22; tive 84; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 AA
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MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                             Pfam; PF00326; Peptidase_S9; 1. PRINTS; PR00862; PROLIGOPTASE.
                                                                                             Bruchhaus I., Heilberg A.;
Submitted (APR-1998) to the
EMBL; AF059278; AAF20264.1;
                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.4%
Best Local Similarity 27.7%
Matches 134; Conservative
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                                                                                                                                                                                                                          InterPro; IPR002470;
                                                                                                                                                                         InterPro; IPR000379;
                                                                                                                                                                                                InterPro; IPR001375;
                                                                                                                                                                                                                                                                                                   665 AA;
                                                 FROM N.A.
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                                                                           STRAIN=HM-1:IMSS
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NCBI_TaxID=5759;
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                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPDGRTLAFISDREGDAA-QLYIMSTE-----GGEARKLTDI-PYGVSKPLWSPDGESI 123
                                                                                                                                                                                                                                                                                                                                                                    Gaps
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                      12 AIVSVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWTHGEKRSTDPRW 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AVKSSHTPRIDP-STGCIYYLS-----DSASSQPVIWKSCESRNDVWLPWERRVGSLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 LVTISLGEGESID----DREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 EMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSLESGDLKQVTPHRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513 GVTGGSYGGFMTNWIVG-QTNRFKAAVTQRSISNWISF------HGVSDIGYFFTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AFTSNKRNGVDFDLYVFDREK------GSVSIVVEGEGIIAAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 SFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 TIAPNYRGSTGYGRRFVHLDDVEKRMDAVR------DVYYAVKAAVEAG-LVDGSRL
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                                                                                                                                                                                                                                                                                                                            Query Match 11.8%; Score 410; DB 1; Length 591; Best Local Similarity 24.9%; Pred. No. 3.4e-20; Matches 167; Conservative 99; Mismatches 244; Indels 162;
                                                                                                                                                                                                                                                                            65756 MW; ECA77CA74A401D67 CRC64;
                                                                                                                                                                                                                                      Pfam; PF00326; Peptidase_S9; 1.
Pfam; PF01738; DLH; 2.
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RYVRLEDEGHGI 567
                                                                                                                                                                                  InterPro; IPR000379;
                                                                                                                                                                                                        InterPro; IPR001375
                                                                                                                                                                                                                       InterPro; IPR002925
                                                                                                                                                                                                                                                                            SEQUENCE
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RESULT 013479

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 MSTEGGEARKLTDIPYGVSKPLWSPDGESILVTISLGEGESIDDREKTEQDSYEPVEVQG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 AKTKSGDIR---FVAYGQSYPNGTAYNEE-LATAPLSSARIYDSIYVRHWDYWLSTTFNA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 HGEKRSTDPRWSPDGRTLAFISDREGD---AAQLYI------93
                                                                                                                                                                                                                                                          Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 AFKSKAPELPKANFTTSYIYLVPHDASETARPINGPDSPGTPKGIKGDSSSPVFSPNGDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 IWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEY------INSFSLSPDEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LALLG-NEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSLIGGAEQRP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beauvais A., Monod M., Debeaupuis J.-P., Diaquin M., Kobayashi H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 TADDITAIVSVTDPQYA-----PDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptidase isolated from Aspergillus fumigatus.";
J. Biol. Chem. 272:6238-6244(1997).
-!- FUNCTION: MAY BE INVOLVED IN METABOLISM OF DIPEPTIDES OR MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Latge J.-P.;
"Biochemical and antigenic characterization of a new dipeptidyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 155;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 19-42; 435-448 AND 593-603
                                                                                                                                                                                            Aspergillus fumigatus (Sartorya fumigata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFFECT HOST DEFENSE MECHANISMS.
-- SUBCELLULAR LOCATION: SECRETED.
-- TISSUE SPECIFICITY: EXPRESSED IN MYCELIA AND CONIDIA.
-- PTH: GLYCOSYLATED.
-- MISCELLANEOUS: THE OPTIMUM PH IS 6.5.
                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-GAT-2000 (TrEMBLrel. 15, Last annotation update)
DIPEPTIDYL-PEPTIDASE V PRECURSOR (EC 3.4.14.-) (DPP V).
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721
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CBS 144.89;
MEDLINE=97197790; PubMed=9045640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L48074; AAB67282.1; -. MEROPS; S09.012; -.
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ACT_SITE
CARBOHYD
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"Secreted alanyl dipeptidyl peptidase (DppV) of Aspergillus oryzae.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFL25190; AAD4177.1; -.
InterPro; IPR000379; -.
SEQUENCE 725 AA; 80383 MW; AD5C7FD79F5D666E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 D-----REGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDGESI------ 123
                                                                                                                                                   :| | : | | : | | : | | 299 RIAYL--QMAAKN.-----YE------SDRRVIHIAEV------GTNKPVQR 330
                                                                                                                                                                                                                                                                                                                                                                     400 I----PEEIQYATEDG--VMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFHEF- 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 GIAAGASFGGFMVNWIQGQDLGRKFKALVSHDG-----TFVGSSKIGTDELFF----IEH 602
                                                                                                                         252 YLALLGNEKEYKNATLSKAWLYDIEOGRLTCLTEMLDVHLADALIGDSLIGGAEORPI-- 309
                                                                                                                                                                                                     -----WIKDSQGFYVIGTDQGSTGIYYI------SIEGLVY 339
                                                                                                                                                                                                                                              331 IASNWDRSPEAVKWSSDGRTLYVTAEDHATGKLFTLPADARDNHKPAVVKHDGSVSSFYF 390
                                                                                                                                                                                                                                                                                     340 PIRLEKEYINSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTIS 399
                                                                                                                                                                                                                                                                                                                                                                                               432 IKGLGPNDIEPLWVDGARTKIHSWIVKPTGFDKNKVYPLAFLIHGGPQGSWGDNWSTRWN 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   567 D----MFEDTEKL--WDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKE 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  603 DFNGTFFEARQNYDRWDCSKPELVAKWSTPQLVVHNDFDFRLSVAEGVGLFNVLQEKGVP 662
                                                                                                                                                                                                                                                                                                                              391 IGSSKSVLISGNSLWSNALYQVAT---PDRPN-------RKLFYAN-----EHDPE 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 -QVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKR 511
241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus oryzae.
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales: Trichocomaceae; mitosporic Trichocomaceae: Aspergillus.
NCBI_TaxID=5062;
                                                                242 MSKAPELPKANLTTSYIFLVPHDGSRVAEPINKRNGPR---TPQGIEGASSSPVFSPDGK
  182 VGTQFNAVFSGTLTKSGDKYSFDGKLKNLVQPVKYAESPYPPFGGSGDYDLSSDGKTVAF
                                         -----SANLTETDDASKPHD----VYIMSLESGDLKQVTPH--RGSFGSSSFSPDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 LGVTGGSYGGFMTNWIVGQT -- NRFKAAVTQRSISNWISFHGVSDIG---YFFTDWQLEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
ALANYL DIPEPTIDYL PEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            621 TKLVRFPNASHNLSRTGHP---RQRIKRLNYISSW 652
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Q9Y8E3;
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LVTISLGE 156 :	KRDGKGLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAFS 197	PDGKWLVFSANLTETDDASKPHDVYIMSLESGDLKQVTPH 237 	RGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDI-EQGRLTCLTEMLDVHL 291 :	ADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEY 347	INSFSLSPDEQHFIASVTKPDRPSELYSIPLGGEEKQLTGANDK 391	FVREHTISIPEEIQYATEDGVMVNGWLMRPAQMEGETTYPLILINIHGGPHMMYGHTYFHE 451	FQVLAAKGYAVYYINPRGSHGYGGEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDP 509 : :    :	510 KRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQRSISNWISFHGVSDIGYFFTD 561	WQLEHDMFEDTEKLMDRSPLKYAANVETPLILHGERDDRCPIEQAEQLFIA 613   :: :	REPDNASH 631   1 : :  .NFPDENH 678	otember 25, 2001, 17:38:52
124IVTISLGE	157KRDGKGLTRGAYAQL'   :   :     189 NAVFSGTLKKSEGKGKATYK	198 PDGKWLVFSANLTETDDASKPHDV	238 RGSFGSSFSPDGRYLALLGNEKE' 1                 291 KGDAGSPVFSPDSKKIAYWQMADE'	292 ADALIGDSLIGGAEQRPIWTKDSQC	348INSFSLSPDEQHFIAS 384 FTDGGVVSAYQLPDSTYLVTSTA	392 FVREHTISIPEEIQYATEDGVMVNG 	452 FOVLAAKGYAVVYINPRGSHGYC : :    :	510 KRLGVIGGSYGGFMINNIVGQT                       555 DNGVAAGASYGGFMINNIQGSDLGF	562WQLEHDMFEDTEKLMDF	614 LKKMGKETKLVRFPNASH 631  ::  ::  ::    LQERGVPSRFLNFPDENH 678	
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Disclosure; Fig 1A-C; 37pp; English.

This DNA sequence encodes serine protease SP1 (YuxL) of Bacillus subtilis. Novel serine proteases SP1, SP2, SP3, SP4 and SP5 (see AAW97789-93) were identified via a RASTA search of Bacillus subtilis genomic nucleic acid sequences. SP1 was identified by its structural homology to the S9 type serine protease dap2 of yeast. SP2, SP3, SP4 and SP5 were identified by their structural and overall amino acid homology to SP1. Host cells in which the naturally occurring gene encoding one or more of SP1, SP2, SP3, SP3, SP4 and SP5 water acid the proteolytic activity is diminished or deleted altogether, can be used for the production of heterologous proteins, e.g. a hormone, enzyme, growth factor, contoking the proteolytic activity is diminished or deleted altogether, can be used for the production of heterologous proteins, e.g. a hormone, enzyme, growth factor, cytokine, protease, carbohydrase, lipase, racemase, epimerase, tautomerase, mutase, transferase, kinase or phosphatase (claimed). SP1, SP2, SP3, SP4 and SP5 can also be produced on a large scale of a manner of the contoking of the compositions such as detergents, bar or liquid scap, dish-care formulations and contact lens cleaning solutions, or for peptide hydrolysis, waste treatment, textile applications, as fusion-cleavage enzymes in protein production, and as animal feed

Sequence 1971 BP; 558 A; 431 C; 524 G; 458 T; 0 other;

ó; 180 240 tacgccccagacggtacccgtgccgcatatgtaaaatcacaagtaaatcaagagaaagat 120 300 300 360 360 420 420 480 480 540 09 09 Gaps 1 atgaaaaagctgataaccgcagacgacatcacagcgattgtctctgtgaccgatcctcaa togtatacatcaaatatatggatctatgaaacgaaaacgggaggatctgttccttggaca catggagaaaagcgaaccgacccaagatggtctccggacgggcgcacgcttgccttt catggagaaaagcgagccgacccaagatggtctccggacgggcgcacgcttgccttt gcaagaaaactgactgatatcccatatggcgtgtcaaagccgctatggtccccggacggt atttctgatcgagaaggcgatgcggcacagctttatatcatgagcactgaaggcggagaa gaatcgattctggtcactatcagtttgggagagggggaaagcattgatgaccgagaaaa gaatcgattctggtcactatcagtttgggagagggggaaagcattgatgaccgagaaaaa 0; 20; Length 1971; Indels .; 0 DB 100.0%; Score 1971; 100.0%; Pred. No. 0; 0; Mismatches Conservative Similarity Query Match Best Local Simi Matches 1971; ( 61 181 181 241 241 301 361 301 361 421 421 481

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hydrolase encoding DNA sequence. The enzyme has the following properties: (a) it hydrolyses an acylpeptide; (b) an optimum temperature of 90.95 degrees Centigrade; (c) an optimum pH of 5.0.6.0; (d) no loss of activity when heated to 95 degrees centigrade for 3 hours at pH 7.5; and (e) a molecular weight of 60 kDa. The enzyme is claimed useful for hydrolysing the amino end of an acylated protein and a peptide at
/product= "Pyrococcus horikoshi acylpeptide hydrolase"
/note= "CDS does not contain a stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding heat-stable amidase from Thermococcus GU5L5 - useful for removing N-terminal amino acids from synthetic peptide(s) \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This novel isolated nucleic acid encodes a 622 amino acid thermostable amidase (see AMW1148) of the archaebacterium Thermoscous GUSLS. It was isolated from a genomic library of GUSLS by screening for amidase activity, and subjecting DNA from a positive clone to PCR amplification (see AAV12888-89). The nucleic acid can be used in the production of amidase in host cells, and to identify related sequences encoding similar enzymes. The encoded amidase is used to remove Arg, Phe or Met from the N-terminus of synthetic peptides or peptidomimetics (claimed). Removal of the N-terminal residue can be done even in the presence of a more reactive ester bond (very difficult to achieve non-enzymatically). The amidase is selective for L-amino acids and can therefore be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used to produce optically active compounds. The protein tolerates temperatures up to at least 70 degc and high concentrations of organic solvent (e.g. over 40% dimethyl sulphoxide) so can cleave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gaggacataatgaacggcatcgaggagttcttcaagctcgaaccgcaggccgacagggag
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/transl_except= (pos:1228..1230, aa:Val)
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                                                                                                                                                                                                                                                                                                                                                                                            (RECO-) RECOMBINANT BIOCATALYSIS INC.
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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be
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                                                                                                                                                                                                                                                               1771 cttttgatactgcatggcgagcgggatgaccgatgcccgatcgagcaggcggagcagctg 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1831 tttategetetgaaaaaaatgggeaaggaaaceaagettgteegtttteegaatgeateg 1890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1732 cacggccacagcgtccgcggaagcccgaggcacaggccgaagcgctacaggctcttcata 1791
1495 gccttctcggacatagggctctggtacgacgtcgaggtcatcgggccaaatccgttagag 1554
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                                                                                          gacacagaaaagctctgggaccggtctcctttaaaatacgcagcaaacgtggagacaccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression; filamentous fungal cell; EST;
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Sequence 659 BP; 162 A; 214 C; 157 G; 126 T; 0 other;
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                                                                                                                                                                                                                                          Oligonucleotide D1835
                                                                                              Local Similarity
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discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on array equals one gene or open reading frame, and organisation of the array equals of the results. AAF07478 to AAF11247 represents ESTs from Fusarium veneratum: AAF11248 to AAF11853 represents ESTs from Aspergillus Fusarium veneratum: AAF11248 to AAF11853 represents ESTs from Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                     niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1358 aggtgctggcggaaaggatacgcggtcgtttatatcaatccgagaggaagccacggct 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1418 acgggcaggaatttgtgaatgcggtcagaggagattatgggggaaaggattatgacgatg 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgatgcaggctgtggatgaggctatcaaacgagatccgcatattgatcctaagcggctcg 1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 aggiettegeegaecagggataegtagtegtegeaeceaaecegaageageagtgget 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 tcggcgatgccetccaggacgccatccaaaaccaatggggaggctaccctacgaagacc 166
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 49.8; DB 21; Length 659; 51.1%; Pred. No. 1.5e-05; iive 0; Mismatches 112; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1538 gigicacgggcggaagciacggaggiittaigaccaaciggaicgicgg 1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 tcgccgcccggtgccagctacggtggcttcatgatcaactggatccaagg 275
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single surface

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1021 attcgtctggaaaaagagtacatcaatagcttttctctttcacctgatgaacagcacttt 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 gittacataaigicaciggagiciggagatettaagcaggitacacetcaicgeggetca 720
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                                                                                                                                                                                                                                                                                  Length 936;
                                                                                                                                                                                                            Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                               340;
                                                                                                                                                                                                                                                                                  Score 48; DB 22; red. No. 7.2e-05;
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Example 6; Page 127; 159pp; English.
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                                                                                                                                                                                                                                                                                                   0.88;
                                                                                                                                                              monitoring gene expression.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 aaatggcttgttttctcagctaatttaactgaaacagatgatgccagcaagccgcatgat 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acatgictiactgagaigctggacgitcatttagcggaigcgctgaitggagaitcaitg 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4%; Score 48; DB 22; Length 936; 0.8%; Pred. No. 7.2e-05; lve 410; Mismatches 340; Indels
                                                                                ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                         (CLIN-) CLINICAL MICRO SENSORS INC.
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2000US-0190259
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                           (first entry)
                                                                                 Electron-transfer group;
                                                     Oligonucleotide D1875
                                                                                                                                                                                                                                                                                                                                WPI; 2001-159728/16
                                                                                                gene expression; ss
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                                                                                                                                                  WO200107665-A2.
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                           24-APR-2001
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9
                                                                                                                          Synthetic.
AAF58254;
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중점

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                                                                                                                                                                                                                                                                                                                                                            cctgaagagattcaatatgctacagaagacggcgtgatggtgaacggctggtgatgagg 1260
1021 attogtotggaaaaagagtacatcaatagottttototttcacotgatgaacagcacttt 1080
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Length 936;

DB 22;

Score 48;

2.48;

01-FEB-2001

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 Similarity 0.8%; Pred. No. 7.2e-05; 6; Conservative 410; Mismatches 340;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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Best Local Similarity 0.8%; Pred. No. 7.2e-05;
Matches 6; Conservative 410; Mismatches 340;
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                                                                                                                   (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                 26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                26-JUL-2000; 2000WO-US20476
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17-MAR-2000; 2000US-0190259.
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   cctgcacaaatggaaggtgagacaacatatccacttattcttaacatacacggcggtccg 1320
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on Nucleic acids containing electron-transfer single surface

Example 6; Page 127; 159pp; English.

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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.

Electron-transfer group; ETM; mismatch; genotyping;

gene expression; ss

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BP

AAF58252 standard; DNA; 936

AAF58252

(first entry)

24-APR-2001

AAF58252;

Oligonucleotide D1835

Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

961 ggcacagatcaaggcagtacgggcatctattatatttcgattgaaggccttgtgtatccg 1020 1021 attcgtctggaaaaagagtacatcaatagcttttctctttcacctgatgaacagcacttt 1080 1141 gaagagaaacagctgactggcgcgaatgacaagtttgtcagggagcatacgatatcaata 1200 attgccagtgtgacaaagccggacagaccgagtgagctttacagtatcccgcttggacag 1140 601 aaatggettgttttetcagetaatttaaetgaaaeagatgatgecageaageegeatgat 660 gtttacataatgtcactggagtctggagatcttaagcaggttacacctcatcgcggctca 720 210 510 570 ttcggatcaagctcattttcaccagacggaaggtatcttgctttgcttggaaatgaaaag 780 gaatataagaatgctacgctctcaaaggcgtggctctatgatatcgaacaaggccgcctc 840 901 atcggtggtgctgaacagcgcccgatttggacaaaggacagccaagggttttatgtcatc 960 Gaps 841 acatgtcttactgagatgctggacgttcatttagcggatgcgctgattggagattcattg cctgcacaaatggaaggtgagacaacatatccacttattcttaacatacacggcggtccg . O 2.4%; Score 48; DB 22; Length 938; 9.8%; Pred. No. 7.2e-05; ve 410; Mismatches 340; Indels catatgatgtacggacatacatatttcatgagttt 1356 Best Local Similarity 0.8%; 6; Conservative Query Match 451 latches 661 91 721 151 1261 õ n ô 묩 ô 님 ठ ㅁ OM 임 ò ם 금 日 8 HO 8 õ õ 님 õ B õ

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16; Conservative 396; Mismatches 343;

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Query Match 2.4%; Score 47.8; DB 2 Best Local Similarity 2.1%; Pred. No. 8.3e-05;

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
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Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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833 geegeeteacatgtettaetgagatgetggaegtteatttageggatgegetgattggag 892
                            1073 agcactttattgccagtgtgacaaagccggacagaccgagtgagctttacagtatcccgc
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17-MAR-2000; 2000US-0190259
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  Length 936;
ch 2.4%; Score 47.8; DB 22; Length 1 Similarity 2.1%; Pred. No. 8.3e-05; 16; Conservative 396; Mismatches 343; Indels
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Best Local Similarity 2.1%;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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2.1%; Pred. No. 8.3e-05;
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                                                                                                                                                    (CLIN-) CLINICAL MICRO SENSORS INC
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                                                                               26-JUL-2000; 2000WO-US20476
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                          Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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Best Local Similarity 2.1%; Pred. No. 8.3e-05;
Matches 16; Conservative 396; Mismatches 343;
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ENTCC88TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 839)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica HMI:INSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
            Description
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/organism="Entamoeba histolytica"
/strain="HM1:IMSS"
/db_zref="texaon:5759"
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Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
/7:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel. 301 838 0200
Email: 910 full setion of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of En
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Best Local Similarity 48.69
Matches 214; Conservative
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Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77.450.) The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                     AZ530780 909 bp DNA GSS 03-NOV-2000
ENTBV92TR Entamoceba histolytica Sheared DNA Entamoceba histolytica
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                                                                                                                                                                                                 Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 909)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
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                03-NOV-2000
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9
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                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
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Class: shotyun
High quality sequence start: 15
High quality sequence stop: 780.
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                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                     AZ530780.1 GI:11084914
                                                             genomic, DNA sequence. AZ530780
                                                                                                                                                                           Entamoeba histolytica.
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Fax: 301 838 0208
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AA071581 327 bp mRNA EST 01-OCT-1996
0028F Pyrococcus furiosus 1-ZAP II library, F Robb Pyrococcus
furiosus cDNA clone 0028 similar to Acylamine Acid releasing enyzme
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,S.T., Szasz,J., Ravel,J., DiRuggiero,J., Fuller,C., Chase,J.W. and
Robb,F.T.
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                                     1441 gtcagaggagattatgggggaaaggattatgacgatgtgatgcaggctgtggatgaggct 1500
                                                                                                          202 AGTATTTGTCCATGGTGGGCCCAAGGGAATGTACGTTATTACTTCAAGTATGAAATGCA 143
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425 ATTGTTTTGCACCCAATTTCCATGGATCAGGAAGTTATGGAGATGCATTTTTAAAAGCA 366
                                                                           365 ATTAGAAAGAATTGGGGAGGATGCCCATTTGAAGATTTAATGAAAGGAATGGATTATTTA 306
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Amersham Life Science, Inc.
Amersham Life Science, 26101 Miles Rd, Cleveland, OH 44128
The 1. 2164649277; 4102348870
Fax: 2163609975; 4102348896
Email: cn288@cleveland.freenet.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Survey of the Genome of the Hyperthermophilic Archaeon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus furiosus
Archaea: Buryarchaeota; Thermococcales; Thermococcaceae;
Pyrococcus
1 (bases 1 to 327)
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Pred. No. 0.0016;
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/organism="Pyrococcus furiosus"
/strain="DSM 3638"."
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/clone="0028"
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AA071581.1 GI:1578969
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Best Local Similarity 51.9%;
Matches 134; Conservative
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Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                    , mRNA sequence.
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Contact Dr. Mary Anne Nelson, Department of Biology, University of New Wexico, Abbuquerque, NM 87131 (e-mail address manelson@unm.edu) regarding clone availability
Seq primer: M13 Universal Reverse Primer
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/dev_stage="sexual"
/lab_host="r. coli strain SoLR"
/note="vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
: 3' end of cDNA cloned into XhoI site of pBluescript
: 120 c 146 g 105 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Neurospora crassa sexual cDNA library, Uni-zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä
                                                                                                                                                                                                                                                                                                                                                                                         BG279712 475 bp mRNA EST 21-FEB-2001 b5e08np.rl Neurospora crassa sexual cDNA library, Uni-zap vector system Neurospora crassa cDNA clone b5e08np 5', mRNA sequence.
                                                                                                 1419 cgggcaggaatttgtgaatgcggtcagaggagattatgggggaaaggattatgacgatgt 1478
1359 ggtgctggcggaaaaggatacgcggtcgtttatatcaatccgagaggaagccacggcta 1418
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
1 (bases 1 to 475)
Kupfer,D., Lai,H., Nelson,M. and Roe,B.
ESTS from a Neurospora crassa Sexual cDNA Library
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                                           142 ATTAATGGCGGCCAAGGGGTACTATATAGTTTACGTTAATCCCAGGGGGAGCAATGGATA 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
Other_ESTs: b5e08np.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
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/db_xref="taxon:5141"
/clone="b5e08np"
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/d_xref="maintains" |
/d_xref="maintains" |
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/d_one_lib="Entamoeba histolytica Sheared DNA" |
/dlone_lib="bentamoeba histolytica Sheared DNA" |
/dlone_lib="bentamoeba histolytica at The Institute for Genomic Research (TIGR), Rockville, MD Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.), The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bjloftus@tigr.org Clones are derived from the Entamoeba histolytica \mbox{HM1:IMSS} sheared
                                                                                                                                                                                                                                                                                                         ENTCD42TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
1479 gatgcaggctgtggatgaggctatcaaacgagatccgcatattgatcctaagcggctcgg 1538
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                                           1480 atgcaggetgtggatgaggetatcaaacgagatecgeatattgatectaageggeteggt 1539
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                                                                                                    1539 tgtcacgggcggaagctacggaggttttatgaccaactggatcgtcgggca 1589
                                                                                                                               Loftus, B. T. Van Akan, S. and Fraser, C. Determination of clone end sequences from Entamoeba HMI:IMSS sheared DNA library Unpublished (200)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200
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Eukaryota; Entamoebidae; Entamoeba.
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Seq primer: M13-Forward
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                      BACR01J16 of RPCI-98 library from Drosophila melanogaster (fruit
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Drosophila melanogaster genome survey sequence TET3 end of BAC
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                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                          fly), genomic survey sequence. AL065414
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/clone_lib="RPCI-98"
/clone="BACR01J16"
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104 c 123 g
                                                                                                                                                                fruit fly.
Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                            BG025910 939 bp mRNA EST 24-JAN-2001
602292657F1 NIH_MGC_86 Homo sapiens CDNA Clone IMAGE:4386711 5',
mRNA sequence.
BG025910
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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49.1%; Pred. No. 0.15;
tive 0; Mismatches 115; Indels 0;
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/lab_host="DH10B (phage-resistant)"
        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_86"
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Location/Qualifiers
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Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 1064)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C.,
Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best blastx match: 'gi|3643594 (AC005395) unknown protein [Arabidopsis thaliana] 316 2e-85'. An open reading frame exists. Insert Length: 1 Std Error: 0.00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/note="3 d 500mM NaCl"
/ 220 c 230 g 311 t 17 others
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                                                                                                                                                                                                                                                                                                                         University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
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0; Mismatches
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/clone_lib="MP"
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                                                                                                                                                                                                                                                                                                        Contact: Michalowski, C.B.
                                                                                                                                                                                                                                                                                                                                                                                         Fax: 520-621-1697
Email: cbm@u.arizona.edu
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         BE036593.1 GI:8331602
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Best Local Similarity 54.5%;
Matches 79; Conservative
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L48-1811T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
NaC1 treatment Mesembryanthemum crystallinum cDNA clone L48-1811
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Buksenbryabathemum crystallinum

Eukaryota; Viridiplantes: Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.

[ Dases 1 to 711)
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/dev_atage="Six week old"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_l:
ECORI; Site_2: Xhol"
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BE036593
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/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:5544"
/clone="L48-1811"
/clone="L48-1811"
/clone="ice plant Lambda Uni-Zap XR e
, 48 hours NaCl treatment"
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Best Local_Similarity 54.5%; Pred, No. 1.3;
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1052 KAKDDADAADAAWAKAKAKDKDKAKKKAD 1081
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High quality sequence stop: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Biochemistry
University of Nevada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jcushman@unr.edu
                                                                                                                                                                                                                            BE130860.1 GI:8578249
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                                                                                                                                                                                    5', mRNA sequence.
BE130860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 775-784-1918
Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACKWARD: T3
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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RECI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potato.
Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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//clone_lib="potato stolon, Cornell University"
//tissue_type="axillary buds of stem explants, swelling stolons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 ggagaggggaaagcattgatgaccgagaaaaaaaagggcaggacagctatgaacctgtt 447
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Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
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/organism="Solanum tuberosum"
/cultivar="Bintje"
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/lab_host="SOLR"
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/db_xref='taxon:5759"
/db_xref='taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pH0S1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Entamoeba histolytica.

Entamoeba histolytica.

Entamoeba histolytica

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Entamoeba histolytica

Entamoeba histolytica

Entamoeba.

Entamoeba.

Entamoeba.

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HMI:IMSS sheared DNA library

Lonpublished (2000)

Contact: Brendan J Loftus

Department of Enkaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 808 0200
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                       Horvath(Laboratory of Plant Breeding, Dept. of Plant Sciences, Wageningen University, The Netherlands). Total RNA was isolated from developing axillary buds of potato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                      nodal stem cuttings cultured on medium for the introduction of tuber formation as described in Bachem al. (Plant Journal 1996). Tissue samples were taken of stages corresponding to growing stolons and the early stages of tuber formation."
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ENTDG10TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 AGTCCTTGGCTTTCCTTTCACTTGGTTATAGCTTGTTGATTGTAAATTATAGAGGCT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 CCTTGGGTTTTGGGGAGGAAGCAGTACAATCTCTTCCTGGGAAAATTGGATCACAGGATG 421
Xhol; RNA was supplied by Christian Bachem & Beatrix
                                                                                                                                                                                                                                                                                                                              Length 513;
                                                                                                                                                                                                                                                                                                                            Score 37.2; DB 122; Length
Pred. No. 5.4;
0; Mismatches 113; Indels
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High quality sequence stop: 844.
Location/Qualifiers
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C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith. H.O. and Venter. J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOSI, Site_l: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark,
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ENTINB4TF Entamoceba histolytica Sheared DNA Entamoceba histolytica
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 926)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                 DB 245; Length 884;
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Tel: 301 838 0200
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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
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High quality sequence stop: 862.
Location/Qualifiers
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AZ689494.1 GI:11826640
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Class: shotgun
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method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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/db_xref="taxon:5759"
/db_clone_lib="Entamoeba histolytica Sheared DNA"
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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ENTHY14TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Determination of clone end sequences
HMI:IMSS sheared DNA library
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The Institute for Genomic Research
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High quality sequence stop: 454
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Contact: Brendan J Loftus
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Loftus, B., Van Aken
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Fax: 301 838 0208
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR15023 of RPCI-98 library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 956)
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DB 219; Length 956;

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Copyright (c) 1993 - 2000 Compugen Ltd.
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2222 2444 388 11111111111111111111111111111111	Application US/09016 6133012 ORMATION: ISAIRAWA, Kaxuhiko Matsui, Ikuo ISAIRA, HITOYSAU KOSUGI, YOSHISUGU HIGUCHI, KATSUHIKO WVENTION: THERMOSTABL WVENTION: THE SAME ENCE: 07898/022001 PILCATION UNMBER: US/ LING DATE: 1998-01-30 DLICATION NUMBER: JAP JING DATE: 1997-01-31 FRO ID NOS: 2 PATCOCCCUS horikoshi CDS (1)(1896)	tch 461; Conservative 6748; 461; Conservative 0998agagaaacagctgactggcg 1
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               1301 tegtegtgatatteteaaateetagagggagegatggetaeggagaggagttegeggat- 1359
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1919 gacagoggatcaagogoctgaattatatcagotcatggtttgatcaacatct 1970
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TITLE OF INVENTION: Amidases
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,646A
FILING DATE: June 17, 1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08664646A Patent No. 5877001 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Charles J. Herron
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 331
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NEW JERSEY
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                                                                                                                                                                                                                        Length 1869;
                                                                                                                                                                                                                      Score 149.8; DB 2; Length
Pred. No. 5.6e-41;
0; Mismatches 322; Indels
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Patent No. 5985646
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TITLE OF INVENTION: Amidases
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                              7.6%;
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1869 NUCLEOTIDES
                                                                                                                                                                                                                                                  Best Local Similarity 52.33
Matches 356; Conservative
                                                                                          TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                TOPOLOGY: LINEAR
                                                                                                                                                    ; MOLECULE TYPE: DNA
US-08-664-646A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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52.3%; Pred. No. 5.6e-41;
tive 0; Mismatches 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664,646
FILLING DATE: June 17, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09261006; Patent No. 6004796
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REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Murphy et al.
TITLE OF INVENTION: Amidases
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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US-09-261-006-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROSELAND
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                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-261-006-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         331400-53
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/066,285
                                                                                                                                                                   E: 3.5 INCH DISKETTE IBM PS/2
                                                                                                                                                                                                                                                                                                                                             08/664,646
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Charles J. Herron
REGISTRATION NUMBER: 28,019
REFRENCE/DOCKET NUMBER: 3314(
TELECOMMULCATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                       6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/664, FILING DATE: June 17, 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                          CITY: ROSELAND
STATE: NEW JERSEY
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                                                                                                                    USA
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                                                                                                                                07068
                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                           COMPUTER:
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1411 cacggctacgggcaggaatttgtgaatgcggtcagaggagattatgggggaaaggattat 1470
                         1315 GAGGACATAATGAACGGCATCGAGGAGTTCTTCAAGCTCGAACCGCAGGCCGACAGGGAG 1374
                                                                               1471 gacgatgtgatgcaggctgtggatgaggctatcaaacgagatccgcatattgatcctaag
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ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
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APPLICATION NUMBER: 08/664,646
FILING DATE: June 17, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08951088
Patent No. 6136583
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TITLE OF INVENTION: Amidases
NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: MS-DOS
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STATE: NEW JERSEY
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-08-951-088-1
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                                                                                                                                                                                                                                                                                      Length 1869;
                                                                                                                                                                                                                                                                                    Query Match
7.6%; Score 149.8; DB 3; Length Best Local Similarity 52.3%; Pred. No. 5.6e-41;
Matches 356; Conservative 0; Mismatches 322; Indels
REFERENCE/DOCKET NUMBER: 331400-53
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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1792 GAGTTCTTCGAGCGCAAGCTC 1812
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                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                 INFORMATION FOR SEQ ID NO: 1:
                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1869 NUCLEOTIDES
                                                                                                                                                                      SINGLE
                                                                                                                                              TYPE: NUCLEIC ACID
                                                                                                                                                                                          TOPOLOGY: LINEAR MOLECULE TYPE: DNA
                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                    US-08-951-088-1
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APPLICANT: DORNER,

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958 atcggcacagatcaaggcagtacgggcatctattatatttcgattgaaggccttgtgtat 1017
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                                                                                                                                                                                                                APPLICANT: Corthesy-Theulaz, Irene
TITLE OF INVENTION: Compositions and Methods Relating to
TITLE OF INVENTION: Drug Discovery and Detection and Treatment of
TITLE OF INVENTION: Gastrointestinal Diseases
NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: Five Palo Alto Square, 3000 El Camino Real
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,776A
                1106 RRRRRRRRRRRRRRRRRRRRRRRRR 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 127;
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Pred. No. 0.085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             Sequence 1, Application US/08834776A Patent No. 6060241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-512-955-3/c; Sequence 3, Application US/08512955; Patent No. 5976536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ashton, Nina M. REGISTRATION NUMBER: 37,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GATTELECOMMUNICATION INFORMATION: TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.8%;
Best Local Similarity 46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-1996
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                                                                         STREET: Five Pal
CITY: Palo Alto
STATE: Californi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94306-2155
                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                        US-08-834-776A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 caagtaaatcaagagaaagattcgtatacatcaaatatatggatctatgaaacgaaaag 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 gacgggcgcacgcttgcctttatttctgatcgagaaggcgatgcggcacagctttatatc 279
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                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                     APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 ctctcctacaaacgggacggcaaagggctgacgagagg 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION: TELEPHONE: (703)836-9300
                                                                                                               E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AGG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29,768
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
APPLICANT: SCHEIFLINGER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 4.8%;
Matches 19; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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.08-232-463-14
                                                                                                                                                  CITY: Alexandria STATE: VA
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                                                                                                            ADDRESSEE:
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GENERAL INFORMATION:

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Sequence 2, Application US/08676967
Patent No. 5747317
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 59.4
Matches 57; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                           COMPUTER READABLE FORM:
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                    New York
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; LOCATION: 581.
US-08-557-139-1
New York
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                                    COUNTRY:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58277300 No. 5827730disk of No. 5827730th America
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58.3%; Pred. No. 0.19;
tive 0; Mismatches 43; Indels
  APPLICANT: Stephens, David S.
APPLICANT: Kahler, Charlene M.
TITLE OF INVENTION: Neisseria Mutants, Lipooligosaccharides
TITLE OF INVENTION: and Immunogenic Compositions
CORRESPONDENCE: 5
CORRESPONDENCE ADDRESS:
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| Sequence 1, Application US/08557139
| Patent No. 5827730
| GENERAL N. F827730
| GENERAL N. F8277300:
| APPLICANT: Pedersen, Oluf
| APPLICANT: Bjorbak, Christian APPLICANT: Frederiksen, Kathrine A. TITLE OF INVENTION: WOTAMT DNA ENCODING INSULIN RECEPTOR TITLE OF INVENTION: SUBSTRATE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE PATENTIN STATEM:

SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,955
FILING DATE: 09-AUG-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REGISTRATION NUMBER: 12-95
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: (303) 499-8089
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                       3E: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis
                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.39
Matches 60; Conservative
                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LOCATION: 1..729
US-08-512-955-3
                                                                                                                                                              CITY: Boulder STATE: Colorado
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                                                                                                                           ADDRESSEE:
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426 gcaggacagctatgaacctgttgaagtgcaaggcctctcctacaaacgggacggcaaagg 485
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APPLICATION NUMBER: US/08/676,967
                                                                 SOFTWARE: Patentin Release #1.0, version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,139
FILING DATE: 12-FEB-1996
CLASSIFICATION: 800
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268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REFERENCE/DOCKET NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4041.204-US
TELEPOMUNICATION INFORMATION:
TELEPERAX: (212) 867-0123
TELEPERAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRRACTERISTICS:
LENGTH: 6152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-098-487-2
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   446 tigaagigcaaggectetectacaaaegggaeggeaaagggetgaegagaggigeteetg 505
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                                                                                                                                                                                                                                                                         Query Match 1.7%; Score 33.4; DB 1; Length 2277; Best Local Similarity 27.3%; Pred. No. 0.82; Matches 81; Conservative 52; Mismatches 164; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
REFERENCE/DOCKET NUMBER: UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/676,974
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Patent No. 5770422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Osman Ph.D., Richard A REGISTRATION NUMBER: 36,627
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
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                                                                               5
                                                                         INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 2277 Base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415)343-4342
INFONMATION FOR SEQ ID NO: 2: SEGUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
                                                                                                                                                                                                MOLECULE TYPE: CDNA
-08-676-967-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94104
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA
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386 tgggagagagaaagcattgatgaccgagaaaaaacagagacagctatgaacctg 445
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                                                                                                                                                                                                                                                                                                                                        446 ttgaagtgcaaggcctctcctacaaacgggacggcaaagggctgacgagaggtgcgtatg 505
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               506 cccagcttgtgcttgtcagcgtaaagtcgggtgagatgaaagagctgacaagtcacaaag 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          803 ARAARMGNGCNGTNAARMGNCCNGCNCCNGCNAARWSNWSNGAYCAYWSNGARGARGAYW 862
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                                                                                                                                                   Query Match 1.7%; Score 33.4; DB 1; Length 2277; Best Local Similarity 27.3%; Pred. No. 0.82; Matches 81; Conservative 52; Mismatches 164; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Science & Technology Law Group: 268 Bush Street, Suite 3200
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UCB96-055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09098487
Patent No. 5917025
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: COLLINS, Kathleen
TITLE OF INVENTION: Human Te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
nucleic acid
                                           ; TOPOLOGY: 11near
; MOLECULE TYPE: CDNA
US-08-676-974-2
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; MOLECULE TYPE: CDNA
US-09-098-487-2
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                   STRANDEDNESS:
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                                                                                                                 446 tigaagigcaaggectetectacaaaegggaeggeaaagggeigaegagaggigegiaig 505
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                                                                                                                                                                                                                                                                  506 cccagcttgtgcttgtcagcgtaaagtcgggtgagatgaaagactgacaagtcacaaag 565
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                                                                                                                                                                                                                                                                                                                                                                                      863 SNGAYYINGARGARWSNGAYWSNAIHGAYGAYGAGGNGARGARYINGCNCARWSNGAYACNW 922
Query Match
1.7%; Score 33.4; DB 2; Length 2277;
Best Local Similarity. 27.3%; Pred. No. 0.82;
Matches 81; Conservative 52; Mismatches 164; Indels 0; Gaps
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APPLICANT: MITSUSHIMA, Kenji
APPLICANT: TAKIMOTO, Akio
APPLICANT: TAKIMOTO, Akio
APPLICANT: TAKIMOTO, Akio
APPLICANT: SONOTANA, Takayasu
TITLE OF INVENTION: Cephalosporin Acetylhydrolase Gene and
TITLE OF INVENTION: Protein Encoded by Said Gene
NUMBER OF SEQUENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 301 N. Washington Street, P. O. Box 747 CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,299
FILING DARTE: 19910422
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APPLICATION NUMBER: JP 2-113483
FILING DATE: 27-APR-1990
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -07-688-299-2
Sequence 2, Application US/07688299
Patent No. 5281525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MURPHY, JR., Gerald M. REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 20-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
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CLASSIFICATION: 435
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                                                                                                1489 gtggatgaggctatcaaacgagatccgcatattgatcctaagcggctcggtgtcacgggc 1548
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                                                                                                                                                                                                                                538 GGAGCCAAGGCGAGGTTTAACCATTGCCGCAGCAGCGCTGTCAGACATTCCAAAAGCC 597
                                                                                                                        0; Gaps
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Best Local Similarity 52.7%; Pred. No. 1.5;
Matches 69; Conservative 0; Mismatches 62; Indels
Score 31.8; DB 1; Length 957;
Pred. No. 1.5;
0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Akio TAKIMOTO
APPLICANT: Shigeo YAGI
APPLICANT: TAKAYASU SONOYAMA
TITLE OF INVENTION: Cephalosporin Acetylhydrolase Gene
TITLE OF INVENTION: and Protein Encoded by Said Gene
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5338676th Washington Street
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOLIWARD.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/980,517A
FTLING DATE: 19921123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19921123
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 3PPLICATION NUMBER: JP 113483/1990
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Virginia
COUNTRY: United States of America
21P: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/07980517A Patent No. 5338676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerald M. Murphy, Jr. RATION NUMBER: 28,977
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REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kenji MITSUSHIMA
APPLICANT: Akio TAKIMOTO
            Query Match 1.6%;
Best Local Similarity 52.7%;
Matches 69; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703-241-1300
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             703-241-2848
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US-07-980-517A-2
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538 GGAAGCCAAGGCGGAGGTTTAACCATTGCCGCAGCAGCTGTCAGACATTCCAAAAGCC 597
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1.6%; Score 31.8; DB 1; Length 2046;
Best Local Similarity 52.7%; Pred. No. 2.7;
Matches 69; Conservative 0; Mismatches 62; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MITSUSHIMA, Kenji
APPLICANT: TAKIMOTO, Akio
APPLICANT: YAGI, Shigeo
APPLICANT: YAGI, Shigeo
APPLICANT: YAGI, Shigeo
APPLICANT: YAGI, Shigeo
APPLICANT: SONOYAMA, Takayasu
TITLE OF INVENTION: Cephalosporin Acetylhydrolase Gene and
INUMBER OF SEQUENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCES: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street, P. O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: RLOPPY disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPATICATION NUMBER: US/07/688,299

FILING DATE: 19910422

CLASSIFICATION NUMBER: JP 2-113483

FILING DATE: 27-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY, JR., GETAID M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 28,977

REFERENCE/COMMUNICATION INFORMATION:

TELEPHONE: (703) 241-1300

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/07688299
Patent No. 5281525
GENERAL INFORMATION:
APPLICANT: MITSUSHIMA, Kenii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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Oy 1609 gccgttaccca 1619
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Db 781 GCGGTTGCCGA 791
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Search completed: September 26, 2001, 08:00:14 Job time: 17436 sec

us-09-462-845-2.rag

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Hydrolases from Gram-positive microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 20; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-347714/29
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1148.499 Million cell updates/sec
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H2 homologue of pr
Sequence of APH36.
Acylamino acid-iso
Human acyl amino a
H1 homologue of pr
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Thermococcus amida
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H2 homologue of
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/SIDSB/gcgdata/geneseqy/geneseqp/Aal984.DaT:*
/SIDSB/gcgdata/geneseqy/geneseqp/Aal985.DaT:*
/SIDSB/gcgdata/geneseqy/geneseqp/Aal986.DaT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS8/gcgdata/geneseq/geneseqp/AA1980.
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                                                                                                                                                                                                                                                                      412676 seqs, 60623988 residues
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                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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		57.5	7.4	160			œ	Human fibroblast a
		U. 14	7.7	7.35				
		243	7.0	771				Rat dipeptidyl pep
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		219	6.3	759				Arabidopsis thalia
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		01.5	5.8	096				Human ORFX ORF2692
		01.5	5.8	968				Arabidopsis thalia
		01.5	5.8	1063				Arabidopsis thalia
		31.5	5.5	487				Arabidopsis challa
		34.5	5.3	710				Himon project
		32.5	5.2	710				Human proly1 endop
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		9.5	5.1	657				Arabidopsis thalia
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Qi	AAY085	553 sta	tandard;	prote	in;	657 AA.		
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KW	Hydrolase; b	ase; b	acteri	bacterial; Gram positive	am p	(1)	YTMA: YITV:	0 4 7
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X X	animal	ford:	YODH;	detection; c	ion;	3	detergent; texti	treatment;
XX		) }		יין אַרי	1017	s; wast	٠.	ge.
SO	Bacillus	s subtil	tilis.					
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PF	19-NOV-	-NOV-1998;	98W	98WO-US2497	973.			
PR	20-NOV-19	1997;	97GI	97GB-002462	. 629			
PA PA	(GEMV)		GENENCOR INT INC	CN L				
XX			1	. )				

Serine protease SP1; YUXL; detergent.

This invention describes novel Gram positive bacterial hydrolases, namely YUXL, YTMA, YIPV, TQKD, YCLE, YTAP, YDEN, YBEK, YFHM, YDJP, YVFQ, YVAM, YQJL, SRFAD, YCGS, YTPA, YBAC, YUII, YODD, YJCH and YODH. The encoding nucleic acid and its fragments, are useful as probes to detect fram-positive hydrolases. The gram-positive microorganisms are used to produce recombinant hydrolases which are useful in cleaning (e.g. detergent) or textile treatment compositions, and in animal feeds. Other uses include peptide hydrolysis, waste treatment and cleavage of fusion proteins.

657 AA; Sequence 0;

PAQMEGETTYPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNA 480 VRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQ 540 481 vrgdyggkdyddvmqavdeaikrdphidpkrlgvtggsyggfmtnwivgqtnrfkaavtg 540 RSISNWISFHGVSDIGYFFTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGERDD 600 361 IASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMR 420 MKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSLESGDLKQVTPHRGS 240 301 IGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHF 360 61 hgekrstdprwspdgrtlafisdregdaaglyimsteggearkltdipygvskplwspdg 120 ESILVTISLGEGESIDDREKTEQDSYEPVEVOGLSYKRDGKGLTRGAYAQLVLVSVKSGE 180 61 HGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDG 120 1 MKKLITADDITAIVSVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWT 60 0; Gaps RCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657 FGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSL 100.0%; Score 3489; DB 20; Length 657; 100.0%; Pred. No. 4.9e-286; Indels ö 0; Mismatches Best Local Similarity 100. Matches 657; Conservative Similarity Query Match 541 421 481 601 421 181 241 ŏ -<u>a</u> 임 õ 뭐 õ õ õ 면 õ 급 õ õ Š a 꿈 굄 d d ð

AAW97789 standard; Protein; 657 AA AAW97789; ~ AAW97789 RESULT

Bacillus subtilis serine protease SP1 (YUXL).

(first entry)

21-MAY-1999

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This polypeptide comprises serine protease SP1 (YUXL) of Bacillus SUbtilis.

Subtilis. Novel serine proteases SP1, SP2, SP3, SP4 and SP5 (see Subtilis. Novel serine protease SP1, SP2, SP3, SP4 and SP5 (see AAW97789-93) were identified via a FASTA search of Bacillus subtilis genomic nucleic acid sequences. SP1 was identified by its spencine brotease dap2 of yeast.

SP2, SP3, SP4 and SP5 were identified by their structural and overall amino acid homology to SP1. Host relia in which the correllance of homology to SP1. Host cells in which the contrainty occurring gene encoding one or more of SP1, SP2, SP3, SP4 or SP5 (see AAX07301-04) is mutated such that the proteolytic of heterologous proteins, e.g. a hormone, enzyme, growth factor, of heterologous proteins, e.g. a hormone, enzyme, growth factor, cytokine, protease, carbohydrase, lipase, racemase, epimerase, cytokine, sp. SP3, SP4 and SP5 can also be produced on a large scale of a microbial host expression system for use in cleaning compositions and contact lens cleaning solutions, or for peptide compositions and contact lens cleaning solutions, as animal feed fusion-cleavage enzymes in protein production, and as animal feed
                                                                                                                                                                                                                                                                                                                                                               Use of serine protease genes from Gram-positive microorganisms - for modification of host cells for the production of heterologous proteins or for producing proteins for use in cleaning compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1A-C; 37pp; English.
                                                                                                                                             98WO-US14647.
                                                                                                                                                                                 97EP-0305232.
                                                                                                                                                                                                                        (GEMV ) GENENCOR INT BV. (GEMV ) GENENCOR INT INC
                                                                                                                                                                                                                                                                                                                     WPI; 1999-132231/11.
                              Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX07301.
                                                                    W09903984-A2
                                                                                                                                               14-JUL-1998;
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                                                                                                           28-JAN-1999.
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181 MKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSLESGDLKQVTPHRGS 240 241 FGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSL 300 121 ESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGE 180 61 HGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDG 120 Gaps ö 100.0%; Score 3489; DB 20; Length 657; 100.0%; Pred. No. 4.9e-286; Live 0; Mismatches 0; Indels 0; Conservative Query Match Best Local Similarity Matches 657; g q qq QΩ δλ οy δ g οy

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657 AA;

Sequence

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hydrolase. The enzyme has the following properties: (a) it hydrolyses an acylepetide; (b) an optimum temperature of 90-95 degrees Centigrade; (c) an optimum pH of 5.0-6.0; (d) no loss of activity when heated to 95 degrees Centigrade for 3 hours at pH 7.5; and (e) a molecular weight of 60 kDa. The enzyme is claimed useful for hydrolysing the amino end of an acylated protein and a peptide at high temperatures.
            IASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMR 420
                                                              PAQMEGETTYPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNA 480
                                                                                                             VRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQ 540
                                                                                                                                                                RSISNWISFHGVSDIGYFFTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLILHGERDD 600
                                                                                                                                                                                                                heat resistant acylpeptide hydrolase and a gene coding it - useful
or hydrolysing the C termini of proteins at high temperature
IGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHF
                                                                                                                                                                                                                                                   601 RCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                                                                                                                                                present sequence represents a Pyrococcus horikoshi acylpeptide
                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus horikoshi acylpeptide hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrococcus horikoshi acylpeptide hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AGEN ) AGENCY OF IND SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                       AAW70508 standard; Protein; 632 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Pages 5-6; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-0018381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97JP-0018381
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus horikoshi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP10210977-A
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                                                                                                                                                                                                                                                                                                                                                                  AAW70508;
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301
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85 EGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDGESILVTISLGEGESIDDREKTEQD 144
                                                                    82 egkeselyviptdggearllakfkygiknlrftedgksiavvtpi-----dvekkgnd 134
                                                                                               145 SYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKWLV 204
                                                                                                                                               205 FSANLTETDDASKP--HDVYIMSLESGDLKQVTPHRGSFGSSSFSP--DGRYLALLGNEK 260
                                                                                                                                                                                               261 EYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSLIGGAEQRPIWTKDSQGFYVI 320
                                                                                                                                                                                                               243 ergiptnahiyhydpktgelkkltkdldrnaynslnsd--vrgsgraelvykegwiyyv- 299
                                                                                                                                                                                                                                                321 GTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHFIA--SVTKPDRPSELYSIPL 378
                                                                                                                                                                                                                                                                                                 379 GQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHG 438
                                                                                                                                                                                                                                                                                                                GPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVD 498
       84
              499 EAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQRSISNWISFHGVSDIGYF 558
                                                                                                                                                                                                                                                                                                                                                                                                                559 FTÖWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWTHGEKRSTDPRWSPDGRTLAFIS--DR
                                                                                                                                                                                                                                                                 Amidase; thermostable enzyme; optically active compound; L-amino acid; peptide; peptidomimetic; archaebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :| || :| :| || 592 krvelaifpgenhdlsrsgkpkhrvkrleliagwmekwl 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 619 KETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded by TGC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW41248 standard; Protein; 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermococcus sp. strain GU5L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US09319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermococcus amidase.
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21;

41; Gaps

Ouery Match 31.7%; Score 1104.5; DB 19; Length 632; Best Local Similarity 39.9%; Pred. No. 1.3e-84; Matches 255; Conservative 126; Mismatches 217; Indels 41;

Query Match Best Local Similarity

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and peptidomimetic(s)
               WPI; 1998-063135/06.
N-PSDB; AAV12887.
         Reid JC,
                                                                                                        Best Local Similarity
                                                                                            622 AA;
                                                                                                           Matches 192;
                                                                                      resistant.
         Murphy D,
                                                                                            Seguence
                                                                                                     Query Match
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRAVIS J.
                                                                                                                                                                                                                                                                                                                                                                                              WO200052147-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Travis J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                        AAB18512;
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                                                                                                                                       AAB18512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                             This protein comprises a novel thermostable amidase of the archaebacterium Thermococcus GU5L5. Its amino acid sequence was deduced from an isolated nucleic acid (see AAV12887). Recombinant amidase can be produced in transformed host cells, especially prokaryotic cells. The amidase is used to remove Arg, Phe or Met from the N-terminus of synthetic peptides or peptidomimetics of claimed). Removal of the N-terminal residue can be done even in the presence of a more reactive ester bond (very difficult to achieve non-enzymatically). The amidase is selective for L-amino acids and can therefore be used to produce optically active compounds. The protein tolerates temperatures up to at least 70 degc and high concentrations of organic solvent (e.g. over 40% degc and high so can cleave bonds that are normally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 EGETTYPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGD 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQRSIS 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      545 NWISFHGVSDIGYFFTDWQ-----LEHDMFEDTEKLWDRSPLKYAANVETPLLILHGER 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 grvnlwlwdgkaervv----tgdhwi------ygldvsdgkallli 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 TKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMRPAQM 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAFIS-DREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDGESILVTISLGEGESID 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 laftcfneekketeiwvadigtlsakkvlstk-nvrsmgwnddsrrllvv----gfkrr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DREKTEQDSYEPVEVQCLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 ddedfvfdddvpvwf-----dnmgffdgekttfwvldteaeeiie-----qfekprf 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 SPDGKW----LVFSANLTETDDASKP-----HDVYIMSLESGDLKQVTPHRGSFGSSSFS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 PDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTE-MLDVHLADALIGD--SLIGGA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 sdgkrillrgkkk--krfisehdwly-lwdgelkpiyegpldvweakltegkvyfltpda 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 EQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHFIASV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 92; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 dprir--gnliaytltkanmkdnkyestvvvedletgs----rrfienasmprispdgrk 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 DPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWTHGEKRSTDPRWSPDGRT 77
                                                                                                                      Nucleic acid encoding heat-stable amidase from Thermococcus GU5L5 -useful for removing N-terminal amino acids from synthetic peptide(s) \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.9%; Score 625; DB 19; Length 622; 29.1%; Pred. No. 3.9e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 113; Mismatches 262;
(RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                                                                                                                                                    Claim 1; Page 39-41; 56pp; English.
                                      Robertson D;
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The present sequence represents a H3 homologue of a prolyl tripeptidase (designated DPP) from Porphyromonas gingivalis. The prolyl tripeptidyl-peptidase has an amidolythic activity, and cleaves a peptide bond in a target polyle having at least 4 amino acids. This bond is between a proline and an amino acid attached to the alpha-carboxyl group end of the proline. The polypeptide is useful for identifying inhibitors. These inhibitors are then useful for reducing the growth of bacterium or for protecting an animal from a periodontal disease such as gingivitis and periodontitis caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prolyl tripeptidyl-peptidase, active analog, fragment or variant useful for identifying its inhibitor which is useful for protecting an animal from a periodontal disease such as gingivitis and periodontitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proly1 tripeptidyl-peptidase; amidolytic activity; periodontal disease;
gingivitis; periodontitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 RSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDGESIL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81; Gaps
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599 DDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                                             546 dyrcpldqslmfynvlkdmgkeayiaifkrgahghsvrgsprhrpkryrlfiefferkl 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 ltpelfmtlsrvsemalspdgktavyavsfpdvktnkatrelftvnldgsgrkgitdtes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.9%; Score 590.5; DB 21; Length 684; 25.8%; Pred. No. 3.8e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 VTISLGEGESIDDREKTEQDSYEPVE-----VQGLSYKR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H3 homologue of prolyl-tripeptidyl peptidase DPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                            AAB18512 standard; protein; 684 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Banbula A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Fig 6; 58pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porphyromonas gingivalis.
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Proly1 tripeptidy1-peptidase; amidolytic activity; periodontal disease;
gingivitis; periodontitis.
217 KPHDVYIMSLESGDLKQVTPHRGSFGSSS---FSPDGRYLALLCNEKEYKNATLSKAWLY 273
                                                                                                  253 tnsdlyiynlasgrthnis--egmmgydtypkfspdgkslawismerdgyesdlkrlfva 310
                                                                                                                          274 DIEDGRLTCLTEMLDVHLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYIS 333
                                                                                                                                       393 VREHTISIPEELQY-ATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGH--TYF 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful
                                                                                                                                                                      334 IE-GLVYPIRLEKEYINSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKF 392
                                                                                                                                                                                      450 HEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDP 509
                                                                                                                                                                                                                                                                                510 KRLGVTGGSYGGFMTNWIVG-QTNRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLEHDM 568
                                                                                                                                                                                                                                                                                                                           162 GLTRGAYAQLVLVSVKSGEMKELTSHKADHG--DPAFSPDGKWLVFSANLTETDDA---S
                                                                                                                                                                                                                                                                                                                                                       569 FED----TEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H2 homologue of prolyl-tripeptidyl peptidase DPP.
                                                                                                                                                                                                                                                                                                                                                                                                                        653 iypdenhwvlq---pqnallfhrtffgwldrwl 682
                                                                                                                                                                                                                                                                                                                                                                                                     625 RFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB18511 standard; protein; 841 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAR-2000; 2000WO-US05551
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29;
                                                                                                       The present sequence represents a H2 homologue of a prolyl tripeptidyl-peptidase (designated DPP) from Porphyromonas gingivalis. The prolyl tripeptidyl-peptidase has an amidolytic activity, and cleaves a peptide bond in a target pollypeptide having at least 4 amino acids. This bond is between a proline and an amino acid attached to the alpha-carboxyl group and of the proline. The polypeptide is useful for identifying inhibitors. These inhibitors are then useful for periodontal disease such as gingivitis and periodontitis caused by
for identifying its inhibitor which is useful for protecting an animal from a periodontal disease such as gingivitis and periodontitis \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 lksillegdttatdvrvvlkpktardssalypnytgkerlslkhmmsgtflsggslsptg 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 kyvltsyrvsrdnkpavtynglrdakgnillnlnekealg--wmphedmlmvir-kegna 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 AQLYIMSTEG-GEARKLTDIPYGVSKPLWSPDGESIL-VTISLGEGE-----SIDDR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 EKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAFSP 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 qsdwrdr-----sqiyllnaesgvygpltfgysttyiydiap 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 krlvafdpmgkgektlvsnlp--esqfrmspdaryylfykqekgpgkdplfirhldpddr 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 121; Mismatches 291; Indels 154; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 DGKWLVFSANLTETDDASKPH---DVYIMSLESGDLKQVTPHRGSFGSSSFSPDGRYLAL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 dskraligt--1stdwtrrpfrfatimeynmetgkadtlitrdpsidaigytpdgkhliv 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 LGNEKEYKNATLS------KAWLYDIEOGRLTCLTEMLDVHLADALIGDSLIGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|: :| |: | |: 427 mgsadafgniglnlksgvtpnsydkgfflfdlstrkataltknfn------psvsag 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 ASVTKPDRPSELYSIPLGQEEKQLTGANDKFV----REHTISI----PEBIQYATEDGVM 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532 ysgqsannadrly-----ridgtkgklvwdlsaeklanidftpardwnytapdgtv 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 AEQRPIWTKDSQGFYVIGTDQGS-TGIYYISIEGL-VYPIRLEKEYINSFSLSPDEQHFI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 rfdr-----knnyyyfraengsrkqlyrldlktleisqiqtgedvvqwfgvaadngavw 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 VNGWLMRPAQMEGETTYPLILNIHGGP----HMMYGHTYFHEFQVLAAKGYAVVYINPRG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 AYVKSQVNQEKDSYTSNIWIYETKTGGSVPWTHGEKRSTDPRWSPDGRTLAFISDREGDA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHGYGQEF ---- VNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTN 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    696 ylqtktdifaaavshagissisnywg---sgy----wgmgystvastdsypwnnpdlyag 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSPLKYAAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTG 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        583 vegwyylppqfdpskkypmlvyyyggtspinrtlegh---yslamyaaqgyvvytlnpsg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526 WIVGQINRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLEHDMFEDTEKL-WD-----
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 841;
                                                                                                                                                                                                                                                                                                                                                                                                                  13.0%; Score 453; DB 21; 23.5%; Pred. No. 2.2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKLITADDITA -- IVSVTDPQYAPD ------
                                                                  Claim 22; Fig 6; 58pp; English.
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                                                                                                                                                                                                                                                                                                           Porphyromonas gingivalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                     841 AA;
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Indels 137;

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Recombinant acyl-peptide hydrolase -used to catalyse hydrolysis of N-acyl peptide(s) or reaction of N-acetyl amino acid donor and acceptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence contains the claimed sequence of acyl-peptide hydrolase (APH) (claim 1, page 11). APH can be used to catalyse the hydrolysis of the N-terminal acyl amino acid of an acylated polypeptide, or the reaction between a derivatised N alpha-acetyl amino acid donor and acceptor with a free alpha-NH2. It can also be used to make refractory proteins susceptible to Edman sequencing or th reduce degradation of proteins to
                                                                                                                                                                                                                                                                                                                                                                       /note="potential site of glycosylation"
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                                                                                                                                                                  'label-claimed protein
                                                                                            Clone APH36.1; acyl-peptide hydrolase
                                                                                                                                          Location/Qualifiers
AAP94265 standard; protein; 783 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEHO-) THE GENERAL HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; ; 21pp; English.
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                                                24-JUN-1990 (first entry)
                                                                     Sequence of APH36.1 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be used therapeutically
                                                                                                                                                                               580..587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              783 AA
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                                                                                                                       Rattus rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1989
                                                                                                                                                                                Active-site
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                      AAP94265;
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Score 396.5; DB 10; Length 783; Pred. No. 1.1e-24;

11.48; 21.78;

Best Local Similarity

Query Match

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563 QLEHDMFEDT------EKLWDRSPLKYAANVETPLLILHGERDBRCPIEQABQLFI 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 625 cmvetgfpysnsclpdlnvweemldkspikylpqvktpvllmlgqedrrvpfkqqmeyyr 684
                                                                                                                                                                                                                                                                                                                                                                                                                                         384 QLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMM 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 YGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKR 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  562
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                                                                                                                                                                                                                                                                                                                       336
                                                                                                                                                                                                                                                                                                                                                                              337 LVYPIRLEKEYINSFSLSPDEQHFIASVTKPDRPSEL---YSIPLGQEE------K 383
                                                                                                                                                                                                                                                                                                                                                                                                          402 sagswkl-----ltidkdlmvaqfstpslppslkvgflpppgkegsvswvsleeae 452
                                                                                                                                                                     169 aesífgtkaldisasddemarpkkpdgaikgdgfvíyedwgetmvsksipvlcvldidsg 228
                                                                                                                                                                                                                                229 nisvlegvpenvspggafwapgdtgvvfvgwwhepfrlgiryctnrrsalyyvdlsggkc 288
                                                                                                                                                                                                                                                            232 KQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHL 291
                                                                                                                                                                                                                                                                                                                                          THGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPD 119
                                                                                                                                          120 GESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSG 179
                                                                                                                                                                                                  180 EMKEL--TSHKADHGDPAFSPDGKWLVFSA-----NLTETDDASKPHDVYIMSLESGDL 231
                                                   93 spsgtmkavlrkaggtvsgeekqfl-evweknrklksfnlsalekhgpvyeddcfgclsw 151
                       22 APDGTRAAYVK---SQVNQEKDSYTSNIW-------IYETKTGGSVPW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPHIDPKRLGVTGGSYGGFMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYFFTDW
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                                                                                                                                                                                                                                                                                                                      292 ADALIGDSLIG-GAEQRPI--WTKDS------QGFYVIGTDQGSTGIYYISIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acylamino acid-isolating enzyme-like polypeptide.
                                                                                                                   152 shseth------llyvaekk-------
Matches 148; Conservative 126; Mismatches
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|685 alkarnvpvrlllypksnhals 706
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Homo sapiens
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20-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 esffqtkaldvtgsddemartkkpdqaikgdqflfyedwgenmvskstpvlcvldiesgn 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 MKEL--TSHKADHGDPAFSPDGKWLVFSA-----NLTETDDASKPHDVYIMSLESGDLK 232
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 21.0%; Pred. No. 3e-24;
Matches 149; Conservative 123; Mismatches 287; Indels 152; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 isvlegvpesvspggafwapgdtgvvfvgwwhepfrlgirfctnrrsalyyvdltggkce 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 QVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 llsdesvavtsprlspdqcrivylrfpslvphqqcgqlclyd----wytrvtsvv-vdiv 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 DALIGDSLIG-GAEQRPI--WTKDS------QGFYVIGTDQGSTGIYYISIEGL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349 prqlgedfsgiycsllplgcwsadsgrvvfdspgrsrqdlfavdtgmgsvtsltaggsgg 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 VYPIRLEKEYINSFSLSPDEQHFIASVTKPDRPSEL---YSIPLGQEEKQLTGANDKFVR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              395 EHTISIP-----EETQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----IYETKTGGSVPWT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 swkl-----avswvsl 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 PHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDE 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500 AIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYF 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: : | | | : : |||: : |||: |||: |||: : | | : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence was obtd. from six clones isolated from a pig liver cDNA library. The clones, lambda AARE 419, 450, 451, 452, 521 and 522 cover the entire sequence of the gene.
                                                                                                               Acylamino acid-isolating enzyme-like polypeptide - prepd. by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               685 eyyrulkarnvpvrlllypksthalsev----evesdsfmnavlwlcthl 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          609 QLFIALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISS--WFDQHL 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 hseth------ilyvaekk-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 APDGTRAAYVKSQ--VNQEKDSYTSNIW-
                                                                                                                                                                                       Claim 1; Fig 2; 10pp; Japanese.
(TAKA-) TAKARA SHUZO KK
                                              WPI; 1991-084340/12.
N-PSDB; AAQ10958.
                                                                                                                                          genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 732 AA;
                                                                                                                                                                                                                                                                                                                               Sequence
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AAR20001
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AAR20001 standard; Protein; 732 AA.

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97 spsgsmkavlrkaggtgpgeekqflevweknrklksfnlsvlekhgpvyeddcfgclsws 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 HGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ESILVTISLGEGESIDDREKTEQDSYEPVE-VQGLSYKRDGKGLTRGAYAQLVLVSVKSG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A human liver cell cDNA library was screened with a cDNA fragment of porcine acyl amino acid acid isolating enzyme-like polypeptide as probe. A positive clone was analysed and sequenced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 11.0%; Score 383; DB 13; Length 732;
Best Local Similarity 21.0%; Pred. No. 1.4e-23;
Matches 147; Conservative 136; Mismatches 287; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 EMKEL--TSHKADHGDPAFSPDGKWLVFSA----NLTETDDASKPHDVYIMSLESGDL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 nisvlegvpenvspggafwapgdagvvfvgwwhepfrlgirfctnrrsalyyvdiiggkc 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 KQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 ellsddslavssprlspdgcrivylgypsliphhgcsglciyd----wytkvtsvv-vdv 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 APDGTRAAYVKS------QVNQEKDSYTSNIW----IYETKTGGSVPWT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 vprqlqenfsgiycsllplgcwsadsqrvvfdsaqrsrqdlfavdtqvgtvtsltaggsg 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 INSFSLSPDEQHFIASVTKPDRPSELY -- SIPLGQEEKQLTGANDKFVREHTISIP---- 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 gswklltidqdlmvaqfstpslpptlkvgflpsagkeqsvlwvs----leeaepipdihw 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 ------EEIQYATEDGVWVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFH 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 girvlqpppeqenvqyarldfeai---llqpgsppdktqvpmvvmphggphssfvtawml 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human acylamino acid-isolating enzyme-like polypeptide - obtd. by culturing transformant contg. introduced recombinant plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 ADALIGDSLIG-GAEQRPI--WTKDSQGFYVIGTDQGSTGIYYISIE-GLVYPIRLEKEY
                                               Human acyl amino acid isolating enzyme-like polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 hseth------llyvaerk-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contg. DNA coding for polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                               90JP-0011718
                                                                                                                                                                                                                                                                                                                                                                                                                                           90JP-0190584
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKA-) TAKARA SHUZO KK.
                                                                                                          recombinant technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-002453/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   732 AA;
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tripeptidy1-peptidase (designated DPP) from Porphyromonas gingivalis. The prolyl tripeptidy1-peptidase has an amidolytic activity, and cleaves a peptide bond in a target polypeptide having at least 4 amino acids. This bond is between a proline and an amino acid attached to the alpha-carboxyl group end of the proline. The polypeptide is useful for identifying inhibitors. These inhibitors are then useful for reducing the growth of bacterium or for protecting an animal from a periodental disease such as gingivitis and periodontitis caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prolyl tripeptidyl-peptidase, active analog, fragment or variant useful
for identifying its inhibitor which is useful for protecting an animal
from a periodontal disease such as gingivitis and periodontitis
                                                                                                                                                                                                                                                                                                                                                                                                                                      Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;
451 EFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVWQAVDEAIKRDPHIDPK 510
                                                                                                                              563 QLEHDMFEDTE---KLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGK 619
                                                                                                                                                             636 pfssdclpdlsvwaemldkspiryipqvktplllmlggedrrvpfkggmeyyralktrnv 695
                       511 RLGVTGGSYGGFMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYFFTDW-----
                                                                                     620 ETKLVRFPNASHNLSRTGHPRQRIKRLNYISS--WFDQHL 657
                                                                                                                                                                                                                     H1 homologue of prolyl-tripeptidyl peptidase DPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYGE-) UNIV GEORGIA RES FOUND INC. (TRAV/) TRAVIS J.
                                                                                                                                                                                                                                                                                                                AAB18510 standard; protein; 541 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Banbula A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; Fig 6; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAR-2000; 2000WO-US05551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0123148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphyromonas gingivalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gingivitis; periodontitis.
                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potempa J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-594181/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTE/) POTEMPA J. (BANB/) BANBULA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200052147-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Travis J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                     AAB18510;
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29;

Gaps

ttch 8.9%; Score 311; DB 21; Length 541; al Similarity 22.9%; Pred. No. 1.1e-17; 143; Conservative 105; Mismatches 223; Indels 154;

Query Match Best Local Si Matches 143;

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Human; T cell activation antigen; CD26; analogues; deletion; soluble; signal peptidase; immune-stimulating; response-stimulating; AIDS; immunosuppression; AIDS-related complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 frisggygkeflragfkqigrkamddvedgvryaisgg-wvdpdriaiygashggyat-- 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                577 ----DRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHN 632
                                                                                                                                                                                                                                                      212 ------kelhklmekefkgkefsvvdydddet-illiavgs-----dklyg 250
                                                                                                                                                                                                                                                                                             349 NSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYAT 408
                                                                                                                                                                                                                                                                                                                                                      409 EDGVMVNGWLMRP-AQMEGETTYPLILNIHGGPHMMYGHTYFH-EFQVLAAKGYAVVIN 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457
                                                                                                                                                                           235 TPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIE----QGRLTCLTEMLDVH 290
                                                                                                                                                                                                      166 kilreifanedydvsglhlsrkrn-----yeidlmayegeksvvvpvsaty 211
                                                                                                                                                                                                                                    291 LADALIGDSLIGGAEQRPIWTKDSQG--FYVIGTDQGSTGIYYISIEGLVYPIRLEKEYI 348
                                                                                                                                                                                                                                                                                                                        251 tyyqfd-----trtkkftllydl-mpq------lkeedmaemrpikfks 287
                                                                                                                                            120 l---kthwddtfg-----viafny----asknkdeayvitnldsdktrivlydlkgn 165
                                                        ---VQGLSYKRDGK-----GLTRGAYAQLVLVSVKSGEMKE 183
                                                                                    60 yklnvvtgeltqlyenkdaanpiggyefdkdgelrgysrlvngieselyykdlatgefrl 119
                                                                                                                   184 LTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHD-VYIM-SLESG------DLKQV 234
91 LYIMSTEGGEARKLTDIPYGVSKPLWSPDG--ESILVTISLGEGESIDDREKTEQDSYEP 148
                     467 PRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 IVGQINRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLEHDMFED-TEKLW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Position of delta3-9 deletion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR54612 standard; Protein; 759 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518 fhreensmelyram---lgffakhl 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633 LSRTGHPRQRIKRLNYISSWFDQHL 657
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(DAND ) DANA FARBER CANCER INST INC 

Tanaka T; Schlossman S, Morimoto C,

WPI; 1994-151317/18.

acid - useful for stimulating immune response, e.g. for treatment of AIDS to counteract immunosuppressive drug, and as vaccine Polypeptide fragments and analogues of CD26 and encoding nucleic

Claim 3; Page 49-52; 85pp; English.

The sequences given in AARS4612-14 represents analogues of the human T analogues pref. lack residues 3-9 or 24-34. These analogues are soluble under physiological conditions and lack enough amino acid residues to render them susceptible to cleavage by signal peptidase. Stimulating therapeutics, eg. they may be used for treatment of AIDS-related complex, other virally or environmentally-induced AIDS-related complex, other virally or environmentally-induced conditions, and certain congenital immune deficiencies. The peptides are be employed to increase immune function which has been impaired by use of immunosupressive drugs, such as certain chemotherapeutic drugs.

Seguence

34; 94 sindysispdggfilleynyvkqwrhsytasydiydlnkrgliteeripnntqwv---- 148 Gaps 66 SIDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLT-----DIPY------ 109 149 ----twspyghklayvwnnd----iyvkiepnlpsyritwtgkedilyngitdwvyeee 199 110 ---GVSKPLWSPDGESILVTISLGEGESIDDRE--KTEQDSYEPVEVQGLSYKRDGKGLT 164 241 ---ypktvrvpypkag------ 270 165 RGAYAQLVLVSV-KSGEMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYI 223 224 MSLESGDLKQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNAT---LSKAWL----- 272 271 -svtnatsiqit-----apasmligdhylc-----dvtwatqerislqwlrriqnysv 317 273 -----YDIEQGRLTCLTEMLDVHLADALIGDSLIGG-AEQRPIWTKDSQGFY-VIGTDQG 325 15 SVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIY------BTKTGGSVPWTHGEKR 65 318 mdicdydessgrwnclvarghiemstt----gwvgrfrpsephftldgnsfykiisneeg 373 326 STGIYYISIB--GLVYPIRLEKEYINSFSLSPDEQHFIASVTK-------- 366 367 ------PDRPSELYSIPLGQEEK--QL------TGANDKFVR--EHTIS 399 434 kvtclscelnper-cqyysvsfskeakyyqircsgpglplytlhssvndkglrvlednsa 492 400 IPEELQYATE-----DGVMVNG---W--LMRPAQMEGETTYPLILNIHGGPHMMYGHTYF 449 450 H---EFQVLAARGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPH 506 553 rlnwatylasteniivasfdgrgsgyggdkimhainrrlgtfevedqieaarqfskmg-f 611 200 vfsaysalwwspngtflaya-----gfndtevplieysfysdeslq-----Query Match
7.8%; Score 272; DB 15; Length 759;
Best Local Similarity 20.4%; Pred. No. 3.6e-14;
Matches 153; Conservative 113; Mismatches 285; Indels 200; ò οy g qq ò δ qq ò q q Q g ŏ Q q ò δ

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507 IDPKRLGVTGGSYGGFMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLE 565
               566 HDMFEDTEKLWDRSPLKYAAN--VETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKL 623
                                                                        666 lptpednldhyrnstvmsraenfkqveyllihgtaddnvhfqqsaqiskalvdvgvdfqa 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C26 is a human T cell antivation antigen originally identified by its reactivity with the MAD Tal. C26 cDNA library was constructed from human PHA-activated T cells using the CDM7vector.The hydrophobic N-terminal of the predicted CD26 polypeptide has the characteristics of a signal sequence of the type II membrane protein, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide fragments of CD26 - are capable of disrupting binding of CD45 and CD26 and thus interfering with T-cell activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= active site of serine protease/esterase
/note= "fits the consensus sequence GXSXG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Cysteine rich region of extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= C-terminal region of extracellular
                                                                                                                                                                                                                                                                                                Human T cell activation antigen; monoclonal antibody Tal.
                                                                                                                                                                                                                                                                                                                                                                                                       /label= N-terminal glycosylated region of extracellular domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "1 N-linked glycosylation site"
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                                                                                                    624 VRFPNASHNL-SRTGHPRQRIKRLNYISSWF 653
                                                                                                                             726 mwytdedhgiasstahghiythmshfikqcf 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catalytic site"
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                                                                                                                                                                                                                                                                        Sequence encoded by human CD26 cDNA.
                                                                                                                                                                                                                                                                                                                                                                             /label= hydrophobic
                                                                                                                                                                                           AAR40909 standard; Protein; 766 AA.
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                    101 sindysispdgqfilleynyvkqwrhsytasydiydlnkrqliteeripnntqwv---- 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ----twspvghklayvwnnd----iyvkiepnlpsyritwtgkediiyngitdwvyeee 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 ---GVSKPLWSPDGESILVTISLGEGESIDDRE--KTEQDSYEPVEVQGLSYKRDGKGLT 164
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                                                                                                                                                                                                                                                              Indels 200; Gaps
                                                                                                                                                                                                                                                                                                        15 SVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIY-----ETKTGGSVPWTHGEKR 65
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reinforced by the observation that potential N-glycosylation sites are located in the carboxy side of the hydropholic core. Therefore the N-terminal 6 AAs are predicted to be cytoplasmic, the next 22 AAs are predicted to transverse the cytoplasmic membrane, and the 738 C-terminal AAs constitute the predicted extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 -----YDIEQGRLTCLTEMLDVHLADALIGDSLIGG-AEQRPIWTKDSQGFY-VIGTDQG
                                                                                                                                                                                                                 7.8%; Score 272; DB 14; Length 766; 20.4%; Pred. No. 3.6e-14;
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                                                                                                                                                                                                                                                                Matches 153; Conservative 113; Mismatches 285;
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                                                                                                                                                           766 AA;
                                                                                                                                                                                                                                                       Local Similarity
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The invention is concerned with molypeptide fragments and analogues of CD26 which have internal deletions (see also AAR54612-14). The analogues pref. lack residues 3 st or 24.34. These analogues are analogues pref. lack residues 3 st or 24.34. These analogues are soluble under physiological conditions and lack enough amino acid residues to render them susceptible to cleavage by signal peptidase. The peptide fragments and analogues are useful as immune or response-simulating therapeutics, eg. they may be used for treatment of disease conditions characterised by immunosupression, eg. AIDS or AIDS-related complex, other virally or environmentally-induced complex, other virally or environmentally-induced complex in certain congenital immune deficiencies. The peptides can be employed to increase immune function which has been impaired by use of immunosupressive drugs, such as certain chemotherapeutic drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----YDIEQGRLTCLTEMLDVHLADALIGDSLIGG-AEQRPIWTKDSQGFY-VIGTDQG 325
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                                 Human; T cell activation antigen; CD26; analogues; deletion; soluble; signal peptidase; immune-stimulating; response-stimulating; AIDS; immunosuppression; AIDS-related complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 vfsaysalwwspngtflaya-----qfndtevplieysfysdeslq------
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide fragments and analogues of CD26 and encoding nucleic acid - useful for stimulating immune response, e.g. for treatment of AIDS to counteract immunosuppressive drug, and as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the human T cell activation antigen CD26.
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Matches 153; Conservative 113; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           Tanaka T;
                                                                                                                                                                                                                                                                                                                    (DAND ) DANA FARBER CANCER INST INC.
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                                                                                                                                  Homo sapiens
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                                                                                                                                                                       WO9409132-A.
              Native CD26.
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325 mdicdydessgrwnclvarghiemstt----gwygrfrpsephftldgnsfykiisneeg 380
                                                                                 381 yrhicyfqidkkdwtfitkgtwevigiealtsdylyyisneykgmpggrnlykiqlsdyt 440
                                                                                                                                    ------PDRPSELYSIPLGQEEK--QL------TGANDKFVR--EHTIS 399
                                                                                                                                                                          441 kvtclscelnper-cqyysvsfskeakyyqlrcs9p91plytlhssvndkqlrvlednsa 499
                                                                                                                                                                                                               400 IPEEIQYATE-----DGVMVNG---W--LMRPAQMEGETTYPLILNIHGGPHMMYGHTYF 449
                                                                                                                                                                                                                                        450 H---EFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVWQAVDEAIKRDPH 506
                                                                                                                                                                                                                                                                                                                                    560 rlnwatylasteniivasfdgrgsgyggdkimhainrrlgtfevedgieaargfskmg-f 618
                                                                                                                                                                                                                                                                                                                                                                             507 IDPKRLGVTGGSYGGEMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLE 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            566 HDMFEDTEKLWDRSPLKYAAN--VETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKL 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     673 lptpednldhyrnstvmsraenfkqveyllihgtaddnvhfqqsaqiskalvdvgvdfqa 732
                                                     326 STGIYYISIE--GLVYPIRLEKEYINSFSLSPDEQHFIASVTK----
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AAW89596 standard; Protein; 931 AA AAW89596

17-MAR-1999 (first entry) AAW89596; 

Saccharomyces cerevisiae dipeptidyl aminopeptidase I.

Prolyl dipeptidyl aminopeptidase; protein hydrolysate; dough; flavour enhancer; palatability; mouthfeel; aroma; crust colour; baking; animal feed additive; hydrolysis.

Saccharomyces cerevisiae.

WO9851803-A1

19-NOV-1998.

98WO-US09629 12-MAY-1998;

97US-0857884. 97us-0062892 16-MAY-1997; 20-0CT-1997;

(NOVO ) NOVO NORDISK BIOTECH INC.

Byun T, Klotz A, Rey MW; Brown K, Blinkovsky A,

New dipeptidyl aminopeptidase from Aspergillus oryzae - used to produce protein hydrolysates enriched in particular amino acids, useful as flavour enhancers, e.g. in doughs WPI; 1999-045232/04.

Example 7; Page 59-61; 77pp; English.

The present sequence represents dipeptidyl aminopeptidase (DPAP) from Saccharomyces cerevisiae. DPAP acts synergistically with aminopeptidase (AP) to hydrolyse polypeptides, producing protein hydrolysate (PH), useful in foods as flavour enhancer, e.g. in baked goods, enriched in:

30; (a) Ala, Arg, Asp, Gly and/or Val, or (b), if the substrate has been deamidated, in Glu (free and/or peptide bound), in which case products are useful as animal feed additives. DAPP can also be used in flavouralso for deactivating enzymes and for converting precursors to mature proteins. DPAP increases the level of hydrolysis of proteins and thus proteins and thus that are resistant to either enzyme used alone. PH have improved solubility, emulsifying and foaming properties, and products containing them have better flavour, palatability, mouthfeel, aroma and crust 220 detfevnlggnrflyegveftvstvqinykldklifgtnlesefrhsskgfywikdlntg 279 55 GSVPWTHGEKRSTD------PRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKL 104 335 te---dgskdifnakpdwiyeeevlasdgaiwwapddsk--avfarfndtsvddirlnry 389 280 niepilppeksddnyelglsklsyahfspaynyiyfvyen----nlflqqvnsgvakkv 334 ----WSPDGESILVTISLGEGESIDDREKTEQ 143 144 DSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKEL-TSHKADHGDPAFSPDGKW 202 445 ispdtfrfei--tdrnskildvkvydipssqmltvrntnsnlfngwiektkdilsippkp 502 --DLKQVTP-- 236 237 --HRGSFGSSSFSPDGRYLALL-------GNEKEYKNATLSKAWLYDIEQG 278 Gaps 503 elkrmdygyidihadsrgfshlfyyptvfakepiqltkgnwevtgngivg----yeyetd 558 279 RLTCLTEMLDV---HLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIE 335 336 GLVYPIRLEKEYINSFSLSPDEQHFIASVTKPDRP------SELYSIPLGQEE 382 602 -----dfelsssaryaisklgpdtpikvagpltrvlnvaeihddsilglt 647 648 k-----dekfkekiknydlpitsyktmvlddgveinyieikpanlnpkkkypilvniygg 702 9 DITAIVSVTDPQYAPDGTRAAYVKSQVNQEKDS--YTSNI-------WIYETKTG 54 559 tifftaneigvmsqhlysisltdsttqntfgslqnpsdkydfy-------- 601 383 KQLTGANDKF---VREHTISIPEEIQYATEDGVWVNGWLMRPAQMEGETTYPLILNIHGG 439 440 PHMMYGHTYF-----HEFQVLAAKGYAVVIINPRGSHGYGQEFVNAVRGDYGGKDYDD 492 493 VMQAVDEAIKRD-PHIDPKRLGVTGGSYGGFMTNWIVGQTN--RFKAAVTQRSISNWISF 549 550 HGV-----SDIGYFFTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGER 598 819 dsvyterymngpsenhegyfevstignfksfeslkrlf-----ivhgtf 862 759 itevtkkfigrnsghideskiaiwgwsyggftslktveldngdtfkyamavapvtnwtly Best Local Similarity 20.18; Pred. No. 8.9e-14; Matches 155; Conservative 108; Mismatches 298; Indels 212; 599 DDRCPIEQAEQLFIALKKMG-KETKLVRFPNASHNLSRTGHPRQRI--KRLNY 648 Length 931; 203 L---VFSANLTETDDASKPHDVYIMSLESG------7.7%; Score 269; DB 20; 20.1%; Pred. No. 8.9e-14; 105 TDIPYGVSKPL----931 AA; Sequence Query Match οy q qq δλ δy g ŏ q δλ q δŏ q ò qq δŏ Op δλ q ò Ωp δ qq δà qq

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prolyl tripeptidyl-peptidase, active analog, fragment or variant useful
for identifying its inhibitor which is useful for protecting an animal
from a periodontal disease such as gingivitis and periodontitis -
                                                                                                                                               Proly1 tripeptidy1-peptidase; amidolytic activity; periodontal disease;
gingivitis; periodontitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 PDG----RTLAFISDREGDAAQ-LYIMSTEGG-----EARKLTDIPYGVSKPLWSPDGE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 7.5%; Score 262.5; DB 21; Length 732; Local Similarity 22.2%; Pred. No. 2.1e-13; hes 159; Conservative 85; Mismatches 261; Indels 211; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a prolyl tripeptidyl-peptidases from Porphyromonas gingivalis, which is designated PTP-A. The prolyl tripeptidyl-peptidase has an amidolytic activity, and cleaves a peptide bond in a target polypeptide having at least 4 amino acids. This bond is between a proline and amino acid attached to the alpha-carboxyl group end of the proline. The polypeptide is useful for identifying inhibitors. These inhibitors are then useful for reducing the growth of bacterium or for protecting an animal from a periodontal disease such as gingivitis and periodontitis caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 -----AYAQLVLVSVKSGEMKELTSHKADHG---DPAFSPDGKWLVF------
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                                                                                                                Amino acid sequence of prolyl-tripeptidyl peptidase PTP-A.
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              AAB18507 standard; Protein; 732 AA
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                                                                                                                                                                                                                                                                                                                03-MAR-2000; 2000WO-US05551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphyromonas gingivalis.
                                                                                      (first entry)
                                                                                                                                                                                                             Porphyromonas gingivalis
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245 SFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRL--TCLTEMLDVHLADALIGDSLIG 302

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629 vidwnryeimygeryf--dapqenpegydaanl-----lkragdlkgrlmlihgaldp-v 680
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                                                                                                                                       339 YPIRLEKEY-----SIPLGO 380
                                                                                                                                                                                                                      381 EEKQL-----TGANDKFVREHTISIPEEIQYATEDGVWVNGWLMRPAQMEGETTYPLI 433
                                                                                                                                                                                                                                                          462 gshtlleaknpdtgyampeirtgti-----maadgqtplyykltmplhfdpakkypvi 514
                                                                                                                                                                                                                                                                                                   434 LNIHGGPHMMY------GHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRG 483
303 GAEQRPIWTKDSQGF---YV-----YV------IGTDQGSTGIYYISIEGLV 338
                                                                                            346 gsnnqfiwqsrrdgwnhlylydttgrlirqvtkgewevtnfagfdpkgtrlyfestea-- 403
                                                                                                                                                                  681 vvwqns11fidacvkartypdyyvypshehnvmgp----drvhlyetitryftdhl 732
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

September 25, 2001, 17:35:13 ; Search time 25.92 Seconds (without alignments) 1930.813 Million cell updates/sec

1 MKKLITADDITAIVSVTDPQ......HPRQRIKRLNYISSWFDQHL 657 US-09-462-845-2 3489 Perfect score: Sequence:

219241 seqs, 76174552 residues Gapop 10.0 , Gapext 0.5 Searched:

BLOSUM62

Scoring table:

Title:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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30	700	3.2	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

RE: E7( Pro C;5	RESULT 1 E70025 Pobele acylaminoacyl-peptidase (EC 3.4.19.1) yuxL - Bacillus subtilis
1, C	C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999 C;Accession: E70025; D25364
R; F C.; A.; Nat	R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Broon, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A; F iec Koe	A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, D. Koningel, G.
A; A	uthors: Lauber, J. Lazarevic, V.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, G. H. Park, V. Dark, V
Ri A;A Ako	eger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Ross, M.; Sadale, Y.; Sato, T.; Scanl uthors: Schlaich, S.; Schroeter, R.; Scoffone, F.; Sekjachi, J.; Sekowska, A.; Sa ochi w
T.; A;A	Winters, F.; Wipat, A.; Yanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida uthors: Yoshikawa. H.F. Zumetein P. Volkis.
A; A	A; Title: The complete genome Sequence of the Gram-positive bacterium Bacillus subtili A; Receive number: A69580; MUID:98044033
A A Y	A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A A A	n.ncarludes: 1.05/ cKUN.> A:Cross.references: B299120; GB:AL009126; NID:92635613; PIDN:CAB15213.1; PID:e11843 A:Experimental source: strain 168
EMB(A) T	K:Parsot, C. EMBO J. 5, 3013-3019, 1986 A:Title: Evolution of biosynthetic nathways.
A; Rt A; Ac	A; Reference number: A91055; MUID: 87080286 A; Accession: D25364
A; K	A;Wolecule type: DNA Residues: 'MPSVPQRQRRAPFFAGDKGVLLETNTCKGGDEYE',3-17,'S',19-24 <par></par>
A; R	#X-LOSS-Teterences: GB:X04663; NID:g40210; PIDN:CAA28272.1; PID:g40213 A:Note: hypothetical fragment that is probably a mistranslation of a portion of the y C:Genetics:
A; Ge	
F; 51	C.ncywolds: nydrolase; omega peptidase F;518,599,631/Active site: Ser, Asp, His #status predicted
Qu Be Ma	Ouery Match Best Local Similarity 100.0%; Pred. No. 8.1e-226; Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Óγ	
QQ	

61 HGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDG 120

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A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50502.1; PID:e151
A;Experimental source: strain Orsay
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable acylaminoacyl-peptidase (EC 3.4.19.1) PABL300 [similarity] - Pyrococcus abys N;Alternate names: acyl-peptide hydrolase (APH); acylamino-acid-releasing enzyme C;Species: Pyrococcus abyssi C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rianonymous, Genoscope submitted to the EMBL Data Library, July.1999 submitted to the EMBL Data Library, July.1999 south the EMBL Data Library, July.1999 south the EMBL Data Library, July.1999 south the EMBL Street of Paragraph 1990 south of the Embler Algorithm 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1990 south 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 PDGESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRD------GKGLT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MMKKISEKDIEKFKLVGN--LDASGKKVVFQVTEISIKENDYFSSIYLYD---GRKVRRF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 EAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQRSISNWISFHGVSDIGYF 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              559 FIDWQLEHDWFEDTEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKLITADDITAIVSVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSV-PW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 G-KEKKVIDFN-KWIKGYILSKPEHFKVKASDGVEIDAWVMKPVNFRKGKKYPAILEIHG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 GPHNMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGGEFVNAVRGDYGGKDYDDVMQAVD 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 GTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHFIA--SVTKPDRPSELYSIPL 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 GQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHG 438
                                                                                                                                                                                       201 FTA---QEDRERKPLISDLYV--LENRKVRKLTP--GKWRILDFLPLDDGSFV-LKANTL 252
                                                                                                                                                                                                                                                          261 EYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSLIGGAEQRPIWTKDSQGFYVI 320
                                                                                                                                                                                                                                                                                              253 ERGIPTNAHIYHYDPKTGELKKLTKDLDRNAYNSLNSD--VRGSORAELVYKEGMIYYV- 309
                                                                                                                                                                                                                                                                                                                                                                                                                          310 ATDGPRANLFRVNLDGKIERVIGGDRSVESFDIG-DYIAFTAQDAVT----PTELKIKRD 364
                                           145 DVH--1IREIPFWFNGVGWIYGKRNVYYLVDDESGKKKRLTPKNLNVDQIRFH-NGR-LY 200
                                                                                                                           205 FSANLTETDDASKP--HDVYIMSLESGDLKQVTPHRGSFGSSSFSP--DGRYLALLGNEK 260
145 SYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKWLV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
31.4%; Score 1096.5; DB 2; Length 631;
Best Local Similarity 38.2%; Pred. No. 1.2e-65;
Matches 258; Conservative 119; Mismatches 233; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 KETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
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C,Keywords: hydrolase; omega peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-631 <KAW>
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A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137
A;Accession: C71137
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A.Experimental source: strain OT3
A.Note: this accession replaces an interim accession for a sequence replaced by GenBank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein PH0863 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14.Aug-1998 #sequence_revision 14.Aug-1998 #text_change 21-Jul-2000
C;Accession: C71137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 31.7%; Score 1104.5; DB 2; Length 642; al Similarity 39.9%; Pred. No. 3.7e-66; 255; Conservative 126; Mismatches 217; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 RSISNWISFHGVSDIGYFFTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGERDD 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 RAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWTHGEKRSTDPRWSPDGRTLAFIS--DR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 KAVFQVTEISLKDDDYFSKLYLYDGKR--VKPFTSGNKDS-NPRFSPNGKLIAFTSKRDK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAQMEGETTYPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSLESGDLKQVTPHRGS 240
                                                                                                                                                                                                                                                                FGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSL 300
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Best Local S
Matches 255
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Db 70 PLTHAETGRGDSAPRWSPDGQNLAFVRSAGEVKAALMLLPLKGGEARRVTHFKNGVSGPQ 129 OY 116 WSPDGESILVTISLGEGESIDDREKTEQDSYEPVEVGGLSYKRDGKGLTRGAY 168   110			QY 624 VRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657  Db 622 VRFPEENHELSRSGRPDRRLTRLNEYFAWLERWL 655  RESULT 5	P/2568 P/	9645783	Ouery Match  27 6%; Score 962.5; DB 2; Length 659;  Best Local Similarity 34.8%; Pred. No. 1.2e-56;  Matches 235; Conservative 120; Mismatches 274; Indels 47; Gaps 18;  Qy 2 KKLITADDITAIVSVTDPQYAPDGTRAAVVKSQNNQEKDSYTSNIWIYETKTGGS 56
Db 115 EDGKEIAV		OY 583 YAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQR 642	EP5551 Probable acyl-peptide hydrolase - Deinococcus radiodurans (strain R1) C;Species: Deinococcus radiodurans C;Date: 03-pec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000	R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Venter, Vorter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999 A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans FA:Reference number: A75250; MUID:20036896 A.Recession: E7551 A.Recession: E7551 A.Roleonle preliminary A:Moleonle two. Days	A;Residues: 1-655 <whi>&gt; A;Cross-references: GB:AE001879; GB:AE000513; NID:g6457832; PIDN:AAF09754.1; PIIC C;Genetics: A;Gene: DR0165 A;Map position: 1</whi>	Query Match Query Match Query Match Dest Local Similarity 36.0%; Pred. No. 8.1e-59; Matches 250; Conservative 102; Mismatches 248; Indels 94; Gaps 19; QY . 8 DDITALVSYTDEQYAPDGTRAAYVESQUVOEKDSYTSNIMIYETKTGGSV 57; Db 12 DSLLALAFPSDPQVSPDGRQVAFVLAQISEEDPARPDKDFARPRYRSGLWLSFGGAAR 69 QY 58 PWTHGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPL 115

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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81302.1; PID:d1045088; PID:g
A;Experimental source: strain K1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable acylamino-acid-releasing enzyme APE2290 - Aeropyrum pernix (strain K1)
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: F72455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 VSDIGYFFTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLF 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 LNIHGGPHMMY -- GHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYD 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 DVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFWTNWIVGQTNRFKAAVTQRSISNWISFHG 551
                                                                                                                                                                                                                                                                                                                                                                                            266 TLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSLIGGAEORPIWTKDSQGFYVIGTDQG 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 IPLGQEEKQLTGANDKFVREHTISIPEEIQYATEDGVM--VNGWLMRPAQMEGETTYPLI 433
177 RHVYVADLAAGRVDRVTAGVAECGGPAWGDDGTLYYPIRRGLDADDRLEWAI----- 228
                                                                                                                                                                                                                                                                                            213 DDASKPHDVYIMSLESGDLKQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNA----- 265
                                                                                                                                                                                                                                                                                                                                           229 -EAATPAD-----SADSTVVTTVEGM------GPTLAVHGSRVAYTTTPADDPTL 271
                                                                                               119 DGESILVTISLGEGESID--DRE---KTEQDSYEPVEVQGLSYK-----RDGKGLTRGAY 168
                                                                                                                                              123 DGDRVAFLOAVRPAERAEELDREHDGEYERDTPDPRVIDROMYRGHTSYRD-----GAR 176
                                                                                                                                                                                               169 AQLVLVSVKSGEMKELTSHKADHGDPAFSPDG---------KWLVFSANLTET 212
                                                                                                                                                                                                                                                                                                                                                                                                                                          272 TQTAVEVEDRDIGATDRLIDGVDRTVAERTAGHA-----PEWGPDGEHLYVCTPDEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 IALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFD 654
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84381
C;Accession: B84381
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Kaller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable, Jung, K.H.; Alam, M.; Freitas, T.
Froc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Reference number: A84160; MUID:20504483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251; Indels 108; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 MINWIVGQINRFKAAVIQRSISNWISFHGVSDIGYFFTDWQLE-HDMFEDTEKLWDRSPL 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             582 KYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQ 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 QYATEDGVMVNGWLMRPAQMEGETT--YPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAV 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400 QVQSPLGGSIDAWILLPPD-AGECSGCLPWILYIHGGPKTSYGYAFIHBFQMLASQGFAV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 VYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDFHIDPKRLGVTGGSYGGF 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 LKQVTPHRG-SFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDV 289
                                                                                                                                                                                                                                                                                                              227 -REKTLIEGLTIAAVAFDPRGRYIAVKANDRKRGLFSHYKIFVYDLNSEEFVCLTCDLDL 285
                                                                                                                                                                                                                                                                                                                                                                       290 HLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYIS-----IEGLVYPIRLE 344
                                                                                                                                                                                                                                                                                                                                                                                                                   286 NTLNTVNSDARGPSCLRGMYW--DDNGHLYYGVHNAGRMYVMKSRPLGEAEAVLDP---S 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 KEYINSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEI 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 SATVDDFSISRGGDTIAYVKMGPTSPPDIY-IYRDDNEYRLTDHNAWFAESRSLAEPVRL 399
                                                                                                                                                                          174 VSVKSGE-MKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKP--HDVYIMSLESGD 230
                                                                                                                                                                                                                         172 ISYPGGEVLLEKGGVNYNIVDFDFAPDDNTIVYAV----STDMKKPFIHKLVLWDLASG- 226
                                                                                                                       117 IKWSSQGSMIGYLSRKPTG-----REWKPYSERDVLEIDRIPVWFDSEGWVFDRYWGLTV 171
     114 PLWSPDGESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.9%; Score 903; DB 2; Length 674; 31.7%; Pred. No. 1.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 31.7%; Fred. No. 1.2e
Matches 223; Conservative 121; Mismatches
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A; Residues: 1-674 <STO>
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Db 111 LEAR-NIRSLEWNDDSRRLLVIGFKRRDDEDFIFEDDVPAMFDNWGFF 157  Oy 165 RGAYAQUVLVSVKSGEMKELTSHKADHGDPAESDDCKWLVFSANLTFT-DDASKPH 219  18 DGEKTTFWIVOTEGENEYLEOFERPRES-GOUNDCEVTWNVPYRDTPRFKYW 210  220 DVYLMSLESGDLKQAPPHRGSEGSSFSPDGRYLALLGN-FEKTWALLSTRAMLYDI 275  211 NITLM	RESULT 9  Pypothetical protein PH0594 - Pyrococcus horikoshii  C;Species: Pyrococcus horikoshii  C;Species: Pyrococcus horikoshii  C;Species: Pyrococcus horikoshii  C;Species: Pyrococcus horikoshii  C;Species: Pyrococcus horikoshii  R;Rawarabayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamamoto, S.; Se-  M; Obfuku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Ogu  A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili  A;Reference number: A;1000; MUID;8344137  A;Reference number: A;1000; MUID;844137  A;Reference number: A;1000; MUID;844137  A;Reference number: A;1000; MUID;844147  A;Reference number: A;1000; MUID;844147  A;Reference number: A;1000; MUID;844147  A;Reference number: A;1000  A;Reference number: A;1000; MUID;844147  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;Reference number: A;1000  A;
Db 2 PSWSPDASKLAFASRRGSGKGEKGSGLYIVG-RGGEPRRVAMFTHGVSEIGWA-SATKVY 59  QY 125 VTISLGBGESIDDREKTEQDSYEDVEVOGISYRRGGRYGOLVLVSVKSGEMKEL 184	PETSOST PETSOS

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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H72474
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A; Residues: 1-591 <KAW>
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A; Status: preliminary
A; Gene: XF2260
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A;Experimental source: strain 9365
B;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Asimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Faranca, A.J.S.
Submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J;Authors: Ferreira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laigi J.D.; Junqueira, M.A.; Madeira, A.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; palmieri, D.P. A;Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z, Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           588 ETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLN 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 DREVAQAKIRNGKV-----YFTLFEEGSVNLYL--WDGEVREIAKGKHW 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 IMGFDA---DERLIYLKETATRPAELYL--WDGEERQLTDYNGLIFKKLKTFEPRHFRFK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SID-LELDGWYIKPEIKEGEKA-PVIVFVHGGPKGMYGYYFKYEMQLMASKGYYIVYVNP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 RGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWI 527
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                                                                                                                                                                                                                                      167 ---QFEKPRFS-SGIWHGDSIVVSV-----PHRDVIPRYFKYWDIYLW--KDGEE 210
                                                                                                                                                                                                                                                                                                                         232 KQVTPHRGSFGSSSF---SPDGRYLALLGN-EKEYKNATLSKAWLYDIEQGRLTCLTEML 287
                                                                                                                                                                                                                                                                                                                                                                                                   211 EKL-----FEKVSFYAIDSDGERILLYGKPEKKYVSEH-DKIYIYD---GEVKGILDDI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 DVHLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEY 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 INSFSLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEELQYA 407
            127 ISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTS 186
                                                                                      120 -----AVGEKRREDEDFIFEDDVPAWF---DNMGFFDGEKTTFWVIDTEGEEVIE--- 166
                                                                                                                                                                187 HKADHGDPAFSPDGKW----LVFSANLTETDDASKPH--------DVYIMSLESGDL 231
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A;Residues: 1-709 <SIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 LILNIHGGPHMYGHTYFHEF--QVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKD 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543 LEDLQKGWAAAQQQYPFLNGDKACALGASYGGYMVYWIAGHWNQ------PWKCL 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 QLVLVSVK-----SGEMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDA-S 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 KPHDVYIMSLESGD----LKQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 MEVQSGKV------REIAPHWDRSADEIALSADGKALYVNADD 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 QGSTGIYYISI-----EGLVYPIRLE--KEYINSFSLSPDEQHFIASVTKPDRPS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 HGEHPLFKVDIASGKVEKWVGEGSVHAPVLAGGKLAFARNSLKSADQIFVTDAVARG--- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 ELYSIPLGQEEKQLTGANDKFVREHTISIPEELQYATEDGVMVNGWLMRPAQMEGETTYP 431
                                                                                                                                                                                                                                                         109 -----VSAPVFSRDGKAVYFLSAKSG-SHQLYVLPVSGGTSRQLTNLAVDIDSYKLSPQG 162
                                                                                                                                                                                                                                                                                                                                   121 ESILVTISL----GEGESIDDREKTEQDS-----YEPVEVQGLSYKRDGKGLTRGAYA 169
                                                                                                                                                                                                                                                                                                                                                                                            163 DRIVFSAGVFQVCGSDLSCTKRKLDEKKNAKASGVVFEQLFVRHWDTWNDGRRNTL-FIA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 TNFDLYRFDVSGHDAPVNLTAANPAWDA--TPWFSADGKMLYYRAMRRPGFEADRFGLME 337
                                                                                                                                                                                                                        61 HGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 599 DDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 DWVALDRVSSPELSPDGAVLVFAKROMDAKYIKASTSVWVQRLQAGTSAAPVRLTPLGWD 108
                                                        Gaps
                                                                                                          9 DITAIVSVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGS------VPWT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 SLPAVGAKPVSVVSAMSAMLDGDVPSKPFGGADHF--VWSPDGHSVVASIRVAGRQEPWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 YDIEQGRLTCLTEMLDVHLADALIGDSLIGGAEQRPIWTK------DSQGFYVIGTD
                                Best Local Similarity 22.7%; Pred. No. 8.2e-24;
Matches 163; Conservative 138; Mismatches 288; Indels 130;
Length 709;
     13.6%; Score 473; DB 2; 22.7%; Pred. No. 8.2e-24;
                 Query Match
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26;

A; Gene: APE2441 C; Genetics

26; 11.8%; Score 410; DB 2; Length 591; 24.9%; Pred. No. 1e-19; Live 99; Mismatches 244; Indels 162; Gaps 72 SPDGRTLAFISDREGDAA-QLYIMSTE-----GGEARKLTDI-PYGVSKPLWSPDGESI 123 113 AFTSNKRNGVDFDLYVFDREK------GSVSIVVEGEGIIAAS-----149 61 APDG-LVAFSTDKDGDERWSIYIAGEDLGVRLVAGEDGSINMIGP------WSPDGRLL 112 124 LVTISIGEGESID----DREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSG 179 180 EMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSLESGDLKQVTPHRG 239 150 -------SWIDGSRLLAVKRNSNLDSDILAVNVYKGEAKVLTRHRG 188 240 SFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDS 299 189 EELNTSPRPIGGGKALFISNMD------SEFTGIALIDLOTGDR 226 300 LIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIEG--LVYPIRLEKEYI----- 348 12 AIVSVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWTHGEKRSTDPRW 71 8 AVKSSHTPRIDP-STGCIYYLS-----DSASSQPVIWKSCESRNDVWLPWERRVGSLEI 60 227 RLVEREQ----W--DVEALEV----SGKTVVYSLNVDGESRVYTTKIDERGSLLQPRPIEG 277 349 ----NSFSLSPDEQHFIA--SVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPE 402 278 LPRGSLLSLDLNEKLGLAVFSLSTPKHGIEIYIAGLGRSASRLTVSPKAWLREDEFVEPE 337 403 EIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFHEF-QVLAAKGYA 461 462 VVYINPRGSHGYGQEFV-----NAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRL 512 396 TIAPNYRGSTGYGRREVHLDDVEKRMDAVR------DVYXAVKAAVEAG-LVDGSRL 445 513 GVTGGSYGGFMTNWIVG-QTNRFKAAVTQRSISNWISF------HGVSDIGYFFTD 561 562 WQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKET 621 Best\_Local Similarity 24.98
Matches 167; Conservative 622 KLVRFPNASHNL 633 556 RYVRLEDEGHGI 567 Query Match òγ ŏ q ò qq ò g ò q οy g δŏ qq Q οy q ð ŏ g g ò

probable acylaminoacyl-peptidase (EC 3.4.19.1) - Aspergillus fumigatus C;Species: Aspergillus fumigatus C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-May-2000 C;Accession: T09631 FSBeauvals, A.; Monod, M.; Svab, J.; Kobayashi, H.; Diaquin, M.; Hovanessian, A.G.; Latg J. Biol. Chem. 272, 6238-6244, 1997 A;Title: Biochemical and antigenic characterization of a new dipeptidyl-peptidase isolat A; Accession:

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-721 <BEA>
A;Cross-references: EMBL:L48074; NID:92340045; PID:92340046

C; Genetics:

A;Introns: 22/2; 39/3; 117/2; 453/3; 528/1; 605/3; 676/2 C;Keywords: hydrolase; omega peptidase

94 MSTEGGEARKL/TDIPYGVSKPLWSPDGESILVTISLGEGESIDDREKTEQDSYEPVEVQG 153 133 AKTKSGDIR---FVAYGOSYPNGTAYNEE-LATAPLSSARIYDSIYVRHWDYWLSTTFNA 188 154 LSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTS--HKADHGDPAF-----SPDGKWL 203 189 VFSGTLKKGHGKNGYS-----LDGELKNLVSPVKNAESPYPPFGGASDYDLSPDGKWV 241 204 VFSANLTETDDAS-----KPHDVYIMSLE-SGDLKQVTPH--RGSFGSSSFSPDGRY 252 Gaps 6 TADDITALVSVTDPQYA-----PDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWT 60 242 AFKSKAPELPKANFTTSYIYLVPHDASETARPINGPDSPGTPKGIKGDSSSPVFSPNGDK 301 253 LALLG-NEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSLIGGAEQRP--- 308 309 IWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEY------INSFSLSPDEQ 358 359 HFIAS------VTKPDRPSELYSIPLGGEEKQLTGANDKFVREHTISIPEEIQYAT 408 15 TALALTPEOLITAPRRSEAIPDPSGKVAVFSTSOYSFETHKRTSWWSLLDLKTGOTKVLT 74 61 HGEKRSTDPRWSPDGRTLAFISDREGD---AAQLYI------93 398 LLVTGSALWTNWNVYTAKPEKGVIKKIASANEIDPELKGLGPSDISEF-----YFO 448 409 EDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFHEF--QVLAAKGYAVVIN 466 467 PRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNW 526 527 IVGQT--NRFKAAVTQRSISNWISFHGVSDIGYFFTD------WQLEHDM----FE 570 509 PIGSTGFGGALTTALQNNWGGAPYDDLVKCWEYVHENLDYVDTDHGVAAGASYGGFMINW 568 569 IQGSPLGRKFKAL------VSHDGTFVADAKVSTEELWFMQREFNGTFWDAR 614 571 DTEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNAS 630 Ouery Match
11.6%; Score 405.5; DB 2; Length 721;
Best Local Similarity 22.3%; Pred. No. 2.8e-19;
Matches 161; Conservative 107; Mismatches 298; Indels 155; 631 н 631 ŏ QΩ Óγ q δλ qq qq δλ δλ QQ ōλ Pρ δλ Dp δ g δ qq

675 H 675 δ

Ωý q δλ

RESULT 13

acylaminoacyl-peptidase (EC 3.4.19.1) - rat
N.Alternate names: acyl-peptide hydrolase; acylamino-acid-releasing enzyme
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 18-Jun-1999
C.Accession: A33706; S07624
E.Kobayashi, K.: Lin, L.W.: Yeadon, J.E.; Klickstein, L.B.: Smith, J.A.
J. Biol. Chem. 264, 8892-8899, 1989
A.Title: Cloning and sequence analysis of a rat liver cDNA encoding acyl-peptide hydr A.Reference number: A33706; MUID:89255359

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22 APDGTRAAYVKSQ--VNQEKDSYTSNIW------
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C; Reywords: blocked amino end; homotetramer; hydrolase; omega peptidase
F; JModified site: blocked amino end (Met) (probably acetylated) #status experimental
F; JModified site: lysine derivative (Lys) #status experimental
F;118,291,443/Modified site: lysine derivative (Lys) #status experimental
F;587,675,707/Active site: Ser, Asp, His #status predicted
                        A.Cross_references: GB:J04733; NID:g202931; PIDN:AAA88506.1; PID:g202932
A.Korss_references: GB:J04733; NID:g202931; PIDN:AAA88506.1; PID:g202932
A.Note: parts of this sequence, including the amino end of the mature protein, were dete
R.Lin, L.W.; Lee, F.J.S.; Smith, J.A.
Nucleic Acids Res. 17, 4397-4400, 1989
A.Mille: Structural organization of the rat acyl-peptide hydrolase gene.
A.Reference number: S07624; MUID:89296508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 DPHIDPKRLGVTGGSYGGFMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYFFTDW 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         574 E-HFDARRVALMGGSHGGFLSCHLIGOYPETYSACIARNPVINIASMMGSTDI----PDW 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       563 QLEHDMFEDT-----EKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFI 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  629 CMVETGFPYSNSCLPDLNVWEEMLDKSPIKYIPQVKTPVLLMLGQEDRRVPFKQGMEYYR 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 YGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEALKR 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 QLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMM 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 PIPGIHWGVRVLHPPPDQENVQYADLDFEAI---LLQPSNPPDKTQVPMVVMPHGGPHSS 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 ADALIGDSLIG-GAEQRPI--WTKDS-------QGFYVIGTDQGSTGIYYISIEG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 VPROLGESFSGIYCSLLPLGCWSADSQRVVFDSAQRSRQDLFAVDTQTGS--ITSLTAAG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 LVYPIRLEKEYINSFSLSPDEQHFIASVTKPDRPSEL---YSIPLGQEE------K 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 SAGSWKL-----LTIDKDLMVAQFSTPSLPPSLKVGFLPPPGKEQSVSWVSLEEAE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 NISVLEGVPENVSPGQAFWAPGDTGVVFVGWWHEPFRLGIRYCTNRRSALYYVDLSGGKC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 KQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEWLDVHL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 ELLSDGSLAICSPRLSPDQCRIVYLQYPCLAPHHQCSQLCLYD----WYTKVTSVV-VDI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 THGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 AESFFQTKALDISASDDEMARPKKPDQAIKGDQFVFYEDWGETWVSKSIPVLCVLDIDSG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 EMKEL--TSHKADHGDPAFSPDGKWLVFSA-----NLTETDDASKPHDVYIMSLESGDL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 SPSGTMKAVLRKAGGTVSGEEKOFL-EVWEKNRKLKSFNLSALEKHGPVYEDDCFGCLSW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 21.7%; Pred. No. 1.1e-18;
Matches 148; Conservative 126; Mismatches 271; Indels 137; Gaps
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Similarity 21.7%; Pred. No. 1.1e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 APDGTRAAYVK---SQVNQEKDSYTSNIW--
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                                                                                                                                                                                                  A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-732 <LIN>
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A; Molecule type: mRNA
A; Residues: 1-732 <KOB>
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|::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       626 -PDWCMVEAGFSYSSDCLPDLSVWAAMLDKSPIKYAPQVKTPLLLMLGQEDRRVPFKOGM 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 EHTISIP------EBIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 EEAEPFPDISWSIRVLQPPPQQEHVQYA---GLDFEAILLQPSNSPEKTQVPMVVMPHGG 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 PHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDE 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWKL-----LIIDRDLMVVQFSTPSVPPSLKVGFLPPAGKEQ----AVSWVSL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 LLSDESVAVTSPRLSPDQCRIVYLRFPSLVPHQQCGQLCLYD----WYTRVTSVV-VDIV 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 PROLGEDFSGIYCSLLPLGCWSADSQRVVFDSPQRSRQDLFAVDTQMGSVTSLTAGGSGG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 VYPIRLEKEYINSFSLSPDEQHFIASVTKPDRPSEL---YSIPLGQEEKQLJGANDKFVR 394
acylaminoacyl-peptidase (EC 3.4.19.1) [validated] - pig
N.Alternate names: acyl-peptide hydrolase; acylamino-acid-releasing enzyme
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 ESFFQTKALDVTGSDDEMARTKKPDQAIKGDQFLFYEDWGENMVSKSTPVLCVLDIESGN 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 MKEL--TSHKADHGDPAFSPDGKWLVFSA-----NLTETDDASKPHDVYIMSLESGDLK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 ISVLEGVPESVSPGQAFWAPGDTGVVFVGWWHEPFRLGIRFCTNRRSALYYVDLTGGKCE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 QVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 DALIGDSLIG-GAEQRPI--WTKDS------QGFYVIGTDQGSTGIYYISIEGL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: EC 3.4.19.1 [validated; MUID:90110044]
C;Superfamily: acylaminoacyl-peptidase
C;Superfamily: acylaminoacyl-peptidase
C;Keywords: acetylated amino end; homotetramer; hydrolase; omega peptidase
F;1/Modified site: acetylated amino end (Met) #status experimental
F;587,675,707/Active site: Ser, Asp, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 HGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 HSETH-----RPKA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 SPSGTMKAVLRKAGGTGTAEEKQFLEVWEKNRKLKSFNLSALEKHGPVYEDDCFGCLSWS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.2%; Score 391; DB 1; Length 732;
Best Local Similarity 21.0%; Pred. No. 2.7e-18;
Matches 149; Conservative 123; Mismatches 287; Indels 152; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------IYETKTGGSVPWT 60
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EYYRVLKARNVPVRLLLYPKSTHALSEVEVESDSFMNAVLWLCTHL 730	Oy Db Oy Db
idase (EC 3.4.19.1) - human acidpeptide hydrolase; acylamino acid releasing enzyme; lung DNF15S2 piens (man) 5; A42257; A30145; A53799 1; H.; Mizutani, S.; Sakiyama, F.; Kato, I.; Tsunasawa, S. 1996 sequence of human acylamino acid-releasing enzyme. 3C4655; MUID:96281126 SNA	
A:Residues: 1-732 <mit> A:Cross-references: DDBB:D38441; NID:9556513; PIDN:BAA07476.1; PID:9556514 A:Cross-references: DDBB:D38441; NID:9556513; PIDN:BAA07476.1; PID:9556514 A:Cross-references: DDBB:D38441; NID:956513; PIDN:BAA07476.1; PID:9556514 B:Scaloni, A.; Jones, W.M.; Barra, D.; Pospischil, M.; Sassa, S.; Popowicz, A.; Manning, B:Scaloni, Chem. 257, 3811-3818, 192 A:Tille: Acylpeptide hydrolase: inhibitors and some active site residues of the human en A:Reference number: A42257; MUID:92156118 A:Reference number: A42257; MUID:92156118 A:Reference number: A42257; MUID:92156118 A:Reference number: A5190-95; J19-126; J30-136, 'A', J38-149; J73-193, 'T', J95-199, 'A', 201-219 A:Residues: 4-18:45-53; 90-95; J19-126; J30-136, 'A', 556-591, 'L', 593; 656-657, 'K', 659-664; 677-6 B:Naylor, S.L.; Marshall, A.; Hensel, C.; Martinez, P.F.; Holley, B.; Sakaguchi, A.Y. A:Tille: The DNF15S2 locus at 3p21 is transcribed in normal lung and small cell lung can A; Reference number: A30145; MUID:89233127</mit>	Db 4 4 4 4 69 69 69 69 69 69 69 69 69 69 69 69 69
','D','114-136,'A',138-167,'K',169-196,'OTKPSRGISLCFWKTGRNMVSKSIPVSACWM','D','114-136,'A',583-604,'RACLRTRDHNASMLGSTDLITGAWW','RL','617-618,63 GB:J03068; NID:g181629; PIDN:AAA35769:L; PID:g181630, a', D:, Jones, W.M.; Manning, J.M. 15076-15084, 1994 Peptide hydrolase. Studies on its thiol groups and mechanism of actic otein 3-55 <sc2> ARR; D3548E; DNF15S2 GDB:L77917; OMIM:102645</sc2>	Oy 62 Db 69 Search c Job time
Observition: hydrolyzes amino-terminal acetylated peptides into peptides having free a C; Superfamily: acylaminoacyl-peptidase C; Superfamily: acylaminoacyl-peptidase C; Keywords: acetylated amino end; blocked amino end; homotetramer; hydrolase; liver; ome F; 1/Modified site: acetylated amino end (Met) #status predicted F; 587/Active site: Ser #status experimental F; 575,707/Active site: Asp, His #status predicted Query Match	
Local Similarity 21.0%; Pred. No. 7.8e-18; les 147; Conservative 136; Mismatches 287; Indels 130; Gaps 24; 22 APDGTRAAVVKS	

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121 ESILVTISLGEGESIDDREKTEQDSYEPVE-VQGLSYKRDGKGLTRGAYAQLVLVSVKSG 179
                           180 EMKEL--TSHKADHGDPAFSPDGKWLVFSA-----NLTETDDASKPHDVYIMSLESGDL 231
                                                                                                             233 NISVLEGVPENVSPGQAFWAPGDAGVVFVGWWHEPFRLGIRFCTNRRSALYYVDLIGGKC 292
                                                                                                                                                                    232 KQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHL 291
                                                                                                                                                                                                         293 ELLSDDSLAVSSPRLSPDQCRIVYLQYPSLIPHHQCSQLCLYD----WYTKVTSVV-VDV 347
                                                                                                                                                                                                                                                         292 ADALIGDSLIG-GAEQRPI--WIKDSQGFYVIGTDQGSTGIYYISIE-GLVYPIRLEKEY 347
                                                                                                                                                                                                                                                                                             348 VPRQLGENFSGIYCSLLPLGCWSADSQRVVFDSAQRSRQDLFAVDTQVGTVTSLTAGGSG 407
                                                                                                                                                                                                                                                                                                                                                                         408 GSWKLLTIDQDLMVAQFSTPSLPPTLKVGFLFSAGKEQSVLWVS----LEEAEPIPDIHW 463
                                                                                                                                                                                                                                                                                                                                           348 INSFSLSPDEQHFIASVTKPDRPSELY--SIPLGQEEKQLTGANDKFVREHTISIP---- 401
                                                                                                                                                                                                                                                                                                                                                                                                                             402 -----EEIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFH 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                           464 GIRVLQPPPEQENVQYA---GLDFEAILLQPGSPPDKTQVPMVVMPHGGPHSSFVTAWML 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 EFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPK 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             511 RLGVTGGSYGGFMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYFFTDW----- 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 OLEHDMFEDTE----KLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGK 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520 ETKLVRFPNASHNLSRTGHPRQRIKRLNYISS--WFDQHL 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 PVRLLLYPKSTHALSEV-----EVESDSFMNAVLWLRTHL, 730
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Search completed: September 25, 2001, 17:37:39 Job time: 146 sec us-09-462-845-2.rpr

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 25, 2001, 17:35:43 ; Search time 16.84 Seconds (without alignments) 1336.452 Million cell updates/sec Run on:

US-09-462-845-2 3489 Perfect score:

1 MKKLITADDITAIVSVTDPQ......HPRQRIKRLNYISSWFDQHL 657 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	pagaa pagaa	rattus	מונים ליונים	S CON								P42558 homo sapien			_		P48147 homo sapien		_			rickettsia			P71505 methylobact				escherich	P27028 flavobacter		<u>~</u>	_	- 8
SUMMARIES		ID	YUXL_BACSU	ACPH_RAT	ACPH PIG	ACPH HITMAN	YL.31 CAPET.		4	DPP4 MOUSE	DPP4 RAT	DPP6 PAT	DDD6 HIMAN	DAP2 VEAST	Debe Boyry	BOTE HARTE	TOLB_HAEIN	PPCE_PIG	FPCE_HUMAN	TOLB PSEAE	TOLB_ECOLI	TOLB_RICPR	PPCE_AERHY	Y174_RICPR	HET I_PODAN	YANA_KHISN	DUNH METEX	PPCF_FLAME	Y L b 3_SYNY 3	TOLB_CHLPN	YIDR_ECOLI	PPCE_FLAME	YA3A_SCHPO	YE91_SYNY3	- 1	YN07_MYCTU
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		Score	3489	396.5	362	384	319.5	272	269	247	242.5	233	224	218.5	211.5	190	179.5	177.5	174 5	170	169.5	100.0	100.0	171	140	142	128 5	137.5	136.5	200	135 5	) —	٦ C		120.0	124
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61 HGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDG 120

34 12.4 3.6 1191 1 Y143_SYNY3 P74442 synechocyst 35 121.5 3.5 561 1 EST4_RAT O64573 actus norv 37 120.5 3.5 5147 1 FAT_DROME P33450 drosophila 38 117.5 3.5 1068 1 TRI_SULSO P95871 sulfolobus 97 116 3.3 4.36 1 SHPL_STAHY P73594 synechocyst 40 115.5 3.3 246 1 DLHH_SYNY3 P73163 synechocyst 41 115.5 3.3 246 1 DLHH_SYNY3 P73163 synechocyst 42 115.5 3.3 1065 1 SED4_YEAST P73163 synechocyst 69116 53.3 1065 1 SED4_YEAST P73163 synechocyst 72 115 3.3 1065 1 SED4_YEAST P73163 synechocyst 73 114.5 3.3 514 1 TUPI_CANAL P56093 candida alb P14870 flavobacter 74 114.5 3.3 428 1 PSG3_HUMAN P14870 flavobacter 7657 homo sapien	RESULT 1 YUXL_BACSU ID YUXL BACSU AC P39839; 032120; DT 01-FEB-1995 (Rel. 31, Created) DT 30-MAY-2000 (Rel. 39, Last sequence update) DT 30-MAY-2000 (Rel. 39, Last annotation update) DT PROBABLE PEPTIDASE YUXL (EC 34, 21 - 1)	YUXL.  Bacillus subtilis.  Bacteria; Firmicutes; Bacimellus/Staphylococcus gr NCBL_TaxID=1423;  [1] SEQUENCE FROM N.A.  STAIN=168;  KURST F., Ogssawara N., Yo		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institution. There are no restrictions on its cuse by non-profit institutions as long as its content is in no way ce entities requires a license agreement (See http://www.isb-sib.ch/announce/cc entities requires algenesent (See http://www.isb-sib.ch/announce/cc EMBL: X99120; CABIS513.1;	je Pe	Best Local Similarity 100.0%; Frod. 00.1.96-218; Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 MKKLITADDITAIVSVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWT 60 bb 1 MKKLITADDITAIVSVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWT 60 bb 1 MKKLITADDITAIVSVTDPQYAPDGTRAAYVKSQVNQEKDSYTSNIWIYETKTGGSVPWT 60
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ACPH_RAT STANDARD; PRT; 732 AA. pp13676; p14320; P70479; p13676; p14320; P70479; p13676; p14320; P70479; p101-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) ACYLAMINO-ACID-RELEASING ENTYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE) (APH) (ACYLAMINOACYL-PEPTIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                      PAQMEGETTYPLILNIHGGPHMMYGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNA 480
                                                                                                                                                                                                                                                                                                                                                                                                                          RSISNWISFHGVSDIGYFFTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGERDD 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 IASVTKPDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYATEDGVMVNGWLMR 420
                                                                                                                                                                                                                                                                                                                                                    IGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIEGLVYPIRLEKEYINSFSLSPDEQHF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                   ESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGE 180
                                                                        MKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSLESGDLKQVTPHRGS 240
                                                                                                                                          FGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSL 300
                                                                                                                                                                                                                Lin L.-W., Lee F.J.S., Smith J.A.;
Lin L.-W., Lee F.J.S., Smith J.A.;
Lin L.-W., Lee F.J.S., Smith J.A.;
Lin L.-W., Lee F.J.S., Smith J.A.;
Nucleic Acids Res. 17.4397-4400(1999).

-I- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
-I- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
AN MACRITATED BAN AND A PEPTIDE WITH A FREE AMINO-TERMINUS.

IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89225359; PubMed=2722805; KDLINE-892255359; Lin L.-W., Yeadon J.E., Klickstein L.B., Smith J.A.; Kobayashi K., Lin L.-W., Yeadon J.E., Klickstein L.B., Smith J.A.; "Cloning and sequence analysis of a rat liver cDNA encoding acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQTNRFKAAVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide hydrolase.";
J. Biol. Chem. 264:8892-8899(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89296508; PubMed=2578023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 QLTGANDKEVREHTISIPEELQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMM 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 PIPGIHWGVRVLHPPPDQENVQYADLDFEAI---LLQPSNPPDKTQVPMYVMPHGGPHSS 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       444 YGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKR 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 FVTAWMLFPAMLCKMGFAVLLVNYRGSTGFGQDSILSLPGNVGHQDVKDVQFAVEQVLQE 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 ADALIGDSLIG-GAEQRPI--WTKDS------QGFYVIGTDQGSTGIYYISIEG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 VPRQLGESFSGIYCSLLPLGCWSADSQRVVFDSAQRSRQDLFAVDTQTGS--ITSLTAAG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406 SAGSWKL-----LTIDKDLMVAQFSTPSLPPSLKVGFLPPPGKEQSVSMVSLEEAE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 ELLSDGSLAICSPRLSPDQCRIVYLQYPCLAPHHQCSQLCLYD----WYTKVTSVV-VDI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 NISVLEGVPENVSPGQAFWAPGDTGVVFVGWWHEPFRLGIRYCTNRRSALXYVDLSGGKC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 KQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 SPSGTMKAVLRKAGGTVSGEEKQFL-EVWEKNRKLKSFNLSALEKHGPVYEDDCFGCLSW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 THGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 AESFFQTKALDISASDDEMARPKKPDQAIKGDQFVFYEDWGETMVSKSIPVLCVLDIDSG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 EMKEL--TSHKADHGDPAFSPDGKWLVFSA-----NLTETDDASKPHDVYIMSLESGDL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 137; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----IYETKTGGSVPW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 LVYPIRLEKEYINSFSLSPDEQHFIASVTKPDRPSEL---YSIPLGQEE-----K
                                              SUBDUIT: HOMOTETRAMER.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
CATALYTIC ACTIVITY: ACYLAMINOACYL-PEPTIDE + H(2)O = ACYLAMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHEMICAL NATURE NOT DETERMINED.
CHEMICAL NATURE NOT DETERMINED.
CHEMICAL NATURE NOT DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 IPDW -> M (IN REF. 2).
81383 MW; 43F234879E10235B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.4%; Score 396.5; DB 1;
ilarity 21.7%; Pred. No. 2.6e-18;
Conservative 126; Mismatches 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 APDGTRAAYVK---SQVNQEKDSYTSNIW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 SHSETH------LLYVAEKK------
                                                                                                                                                                                                                                                                                                                                                                                          Promis PF00326; Peptidase_S9; 1.
PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
                                                                                                                                                                                                                                                                                            EMBL; X14915; CAA33040.1; ALT_SEQ.
PIR; S07624; S07624.
                                                                                  PROLYL OLIGOPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                EMBL; J04733; AAA88506.1;
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001375; -. InterPro; IPR002471; -.
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707
625
732 AA;
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Best Local Similarity
                              ACID + PEPTIDE.
                                                                                                                                                                                                                                                                                                                                        MEROPS; S09.004; -
                                                                  SIMILARITY:
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                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ACYLAMINO-ACID-RELEASING ENZYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE)
504 DPHIDPKRLGVTGGSYGGFMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYFFTDW 562
                      629 CMVETGFPYSNSCLPDLNVWEEMLDKSPIKYIPQVKTPVLLMLGQEDRRVPFKQGMEYYR 688
                                                                563 QLEHDMFEDT------EKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFI 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitta M., Asada K., Uchimura Y., Kimizuka F., Kato I., Sakiyama F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C; ALSO KNOWN AS THE PROLYL OLIGOPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
FERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINGS.
IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CATALYTIC ACTIVITY: ACYLAMINOACYL-PEPTIDE + H(2)O = ACYLAMINO
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The primary structure of porcine liver acylamino acid-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM (BY SIMILARITY). CHARGE RELAY SYSTEM (BY SIMILARITY).
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(BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY S
0178D40E049A604C CRC64;
                                                                                                                                                                                                                                                       732 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme deduced from cDNA sequences.";
J. Blochem. 106:548-551(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00326; Peptidase_S9; 1.
PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90110044; PubMed=2691504;
                                                                                                                                                     613 ALKKMGKETKLVRFPNASHNLS 634
                                                                                                                                                                                                                                                                                                                                                      (APH) (ACYLAMINOACYL-PEPTIDASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001375; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            587
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MEROPS; S09.004; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9823;
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707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsunasawa S.;
                                                                                                                                                                                                                                                    ACPH_PIG
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                RESULT
ACPH_PIG
                               q
                                                                                              Db
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Gaps

Indels 152;

Query Match 11.3%; Score 395; DB 1; Length 732; Best Local Similarity 21.1%; Pred. No. 3.2e-18; Matches 150; Conservative 122; Mismatches 287; Indels 1:

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97 SPSGTMKAVLRKAGGTGTAEEKQFLEVWEKNRKLKSFNLSALEKHGPVYEDDCFGCLSWS 156
                                                                                                                                            61 HGEKRSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDG 120
                                                                                                                                                                                                                                                                                                121 ESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGE 180
                                                                                                                                                                                                                                                                                                                                                                        174 ESFFQTKALDVTGSDDEMARTKKPDQAIKGDQFLFYEDWGENMVSKSTPVLCVLDIESGN 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 MKEL--TSHKADHGDPAFSPDGKWLVFSA-----NLTETDDASKPHDVYIMSLESGDLK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 ISVLEGVPESVSPGQAFWAPGDTGVVFVGWWHEPFRLGIRFCTNRRSALYYVDLTGGKCE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ACYLAMINO-ACID-RELEASING BAZYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE)
(APH) (ACYLAMINOACYL-PEPTIDASE) (DNF1552 PROTEIN).
                                                                                                                                                                                                                                            ------RPKA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 QVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCLTEMLDVHLA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 LLSDESVAVTSPRLSPDQCRIVYLRFPSLVPHQQCGQLCLYD----WYTRVTSVV-VDIV 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 DALIGDSLIG-GAEQRPI--WTKDS------QGFYVIGTDQGSTGIYYISIEGL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 PRQLGEDFSGIYCSLLPLGCWSADSQRVVFDSPQRSRQDLFAVDTQMGSVTSLTAGGSGG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 SWXL-----AVSWVSL 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 EHTISIP------EELQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 EEAEPFPDISWSIRVLOPPPQOEHVQYA---GLDFEAILLQPSNSPEKTQVPMVVMPHGG 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 AIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQ-INRFKAAVTQRSISNWISFHGVSDIGYF 558
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                ---IYETKTGGSVPWT 60
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NayLor S.L., Marshall A., Hensel C., Martinez P.F., Holley B.,
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22 APDGTRAAYVKSQ - - VNQEKDSYTSNIW-
                                                                                                                                                                                                                        157 HSETH------LLYVADKK----
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY DUE TO
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                                                                                                                                                                                        Erlandsson R., Boldog F., Persson B., Zabarovsky E.R., Allikmets R.L., Sumedi J., Klein G., Joernvall H.; "The gene from the short arm of chromosome 3, at D3F15S2, frequently deleted in renal cell carcinoma, encodes acylpeptide hydrolase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genetic relationship between acylpeptide hydrolase and acylase, two hydrolytic enzymes with similar binding but different catalytic
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            The DNF1552 locus at 3p21 is transcribed in normal lung and small
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                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91172778; PubMed=2006156;
Jones W.M., Scaloni A., Bossa F., Popowicz A.M., Schneewind O.,
Manning J.M.;
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PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
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EMBL; J03068; AAA35769.1; ALT_FRAME.
                                                                                                                                                                     MEDLINE=91319413; PubMed=1861871;
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                                                           cell lung cancer.";
Genomics 4:355-361(1989).
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Sakaguchi A.Y.;
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Deligner Berks M., Mederson K., Baynes C., Berks M., MEDLINE=94150718; Pubbled=7906398; Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Wilson R., Ainscough R., Anderson K., Engeld J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Tulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laissten N., Lightning J., Lidyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Sulston J., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 ADALIGDSLIG-GAEQRPI--WTKDSQGFYVIGTDQGSTGIYYISIE-GLVYPIRLEKEY 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 VPROLGENFSGIYCSLLPLGCWSADSQRVVFDSAQRSRQDLFAVDTQVGTVTSLTAGGSG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 INSFSLSPDEQHFIASVTKPDRPSELY--SIPLGQEEKQLTGANDKFVREHTISIP---- 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  408 GSWKLLTIDQDLMVAQFSTPSLPPTLKVGFLPSAGKEQSVLWVS----LEEAEPIPDIHW 463
                                                                                                   121 ESILVTISLGEGESIDDREKTEQDSYEPVE-VQGLSYKRDGKGLTRGAYAQLVLVSVKSG 179
                                                                                                                                                                                174 ESFFQTKALDVSASDDEIARLKKPD-QPIKGDQFVFYEDWGENMVSKSIPVLCVLDVESG 232
                                                                                                                                                                                                                                                              180 EMKEL--TSHKADHGDPAFSPDGKWLVFSA-----NLTETDDASKPHDVYIMSLESGDL 231
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Rhabditidae; Peloderinae; Caenorhabditis.
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01-FBB-1994 (Rel. 28, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 86.0 KDA PROTEIN F44B9.1 IN CHROMOSOME III.
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157 HSETH-----LLYVAERK-
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616 KMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                 -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C; ALSO KNOWN AS THE PROLYL OLIGOPEPTIDASE FAMILY. STRONG, TO ACYLAMINO-ACID-RELEASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 DPRW-----SPDGRTLAFISDREGDAAQLYIMSTEGGEARKLT-DIPYGVSKPLWSPDGE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 DPKYSSVSLSPDAKQVGYVAPDENGIRNVFTRCSSCSYSROVTFETEHPILNYVWTAIPD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 SILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYA----QLVLVSVK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 VILFT-------ODNHGDENTR--IYK---KNISATAIAADKTORVVISEK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 SGEMKELTSHKADHGDPAFSPDGKWLVFSANL-TET-----DDASKPHDVYIMSLESGD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 -------PMVKAMILSNNLISETVLIGMNDENPALHNIYAFNCQTDE 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 GTDQGS-----TGIYY-----ISIEGLVYPIRLEKE-YINSFSL 353
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589 GADISD-----EEGRQSLQSRSPLFFADRVTKPIMIIQGANDPRVKQAESDQFVAALE 641
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7766F0AAF2650364 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 129; Mismatches 247; Indels 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.2%; Score 319.5; DB 1
20.4%; Pred. No. 2.6e-13;
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657 657 C
761 AA; 85963 MW;
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                Nature 368:32-38(1994).
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TISSUB-Peripheral blood, MEDINE-9325476; PubMed-1352530; Tanaka T., Camerini D., Seed B., Torimoto Y., Dang N.H., Kameoka J., Dahlberg H.N., Schlossman S.F., Morimoto C.; "Cloning and functional expression of the T cell activation antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95012454; PubMed=7927537; Abbort C-A., Baker E., Sutherland G.R., McCaughan G.W.; Genomic organization, exact localization, and tissue expression of the human CD26 (dipeptidy) peptidase IV) gene."; Immunogenetics 40:331-338(1994).
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                                                                                                                                                                                                                          01-507.1992 (Rel. 23, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DIPPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD25) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE_92329551; PubMed=1352704; Misumi Y., Hayashi Y., Arakawa F., Ikehara Y.; Misumi Y., Hayashi Y., Arakawa F., Ikehara Y.; Molecular cloning and sequence analysis of human dipeptidy peptidase IV, a serine proteinase on the cell surface."; Biochim. Biophys. Acta 1131:333-336(1992).
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Trotot P., Barbat A.;
642 KKHIPVTYLLYPDEGHGVRK---PQNSMEQHGHIETFLQQCL 680
                                                                                                                                                                                PRT;
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MEDLINE=91024044; PubMed=1977364;
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J. Immunol. 150:2090-2090(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. 149:481-486(1992).
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P27487;
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                                                                                                             RESULT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   PTM: THE SOLUBLE FORM (SDPP) DERIVES FROM THE MEMBRANE FORM (MDPP) PTM: THE SOLUBLE FORM (SDPP) BY PROTECLYTIC PROCESSING.
SIMILARITY: BELONGS TO PREPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLYL OLIGOPEPTIDASE FAMILY.
DATABASE: NAME-PROW; NOTE-CD guide CD26 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd26.htm".
                                                                                                                                                    Houghton A.N.;
"A marker for neoplastic progression of human melanocytes is a cell
surface ectopeptidase.";
surface ectopeptidase.";
-i. EVO. 177:1135-1143(1993).
-i. FUNCTION: REMOVES N-TERMINAL DIPEPTIDES SEQUENTIALLY FROM
POLYPEPTIDES HAVING UNSUBSITUTED N-TERMINI PROVIDED THAT THE
PENULTIMATE RESIDUE IS PROLINE.
-i. CARALYTIC ACTIVITY: DIPEPTIDXL-POLYPEPTIDE + H(2)O = DIPEPTIDE.
POLYPEPTIDE.
                                                                                                                                                                                                                                                                  SUBGNIT: HOMODIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS IN
MEDLINE=96067599; PubMed=7487939;
Boehm S.K., Gum J.R. Jr., Erickson R.H., Hicks J.W., Kim Y.S.;
"Human dipeptidyl peptidase IV gene promoter: tissue-specific
regulation from a TATA-less GC-rich sequence characteristic of
                                                                                                                                Morrison M.E., Vijayasaradhi S., Engelstein D., Albino A.P.
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AAB60646.1; JOINED.
                                                                                                                rISSUE=Kidney;
MEDLINE=93210468; PubMed=8096237;
                                                       housekeeping gene promoter.";
Biochem. J. 311:835-843(1995).
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CAA43118.1;
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                                                                                                 PARTIAL SEQUENCE.
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400 IPEELQYATE-----DGVMVNG---W--LMRPAQMEGETTYPLILNIHGGPHMMYGHTYF 449
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                                                                                                                                 (BY SIMILARITY).

CYTOPLASMIC (POCENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
CHARGE RELAX SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 ----TWSPVGHKLAYVWNND-----IYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 ---GVSKPLWSPDGESILVTISLGEGESIDDRE--KTEQDSYEPVEVQGLSYKRDGKGLT 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 SINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWV---- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285; Indels 200; Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 766;
                                                                                            MEMBRANE FORM OF DPP (MDPP)
Interpro; IPR002471; -
Pfam; PF00930; DPPIV_N-term; 1.
Pfam; PF00326; Peptidase_S9; 1.
PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
Hydrolase; Aminopeptidase; Dipeptidase; Serine protease;
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                                                                                                                SOLUBLE FORM OF DPP (SDPP)
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766 AA;
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Best Local Similarity
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560 RLNWATYLASTENIIVASFDGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMG-F 618
                                                 507 IDPKRLGVTGGSYGGFMTNWIVGQ-TNRFKAAVTQRSISNWISFHGVSDIGYFFTDWQLE 565
                                                                                  619 VDNKRIAIWGWSYGGYVTSMVLGSGSGVFKCGIAVAPVSRWEYYDSV-----YTERYMG 672
                                                                                                                    566 HDMFEDTEKLWDRSPLKYAAN--VETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKL 623
                                                                                                                                                    673 LPTPEDNLDHYRNSTVMSRAENFKQVEYLLIHGTADDNVHFQQSAQISKALVDVGVDFQA 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (In) Gething M.-J., Novick P., Stevens T.H., Rothblatt J. (eds.);
Guidebook to the yeast secretory pathway, pp.1-1, Oxford University
Press, Oxford (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
DIPEPTIDYL AMINOPEPTIDASE A (EC 34.14.-) (DPAP A) (YSCIV).
STE13 OR YCII OR YOR519C OR YOR50-9.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina: Saccharomycetaies; Saccharomycetaies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anna-Arriola S.S., Herskowitz I.; "Isolation and DNA sequence of the STB13 gene encoding dipeptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. LYSOSOME-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galisson F., Dujon B.;
"Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV of the yeast Saccharomyces cerevisiae.";
Yeast 12:877-885(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: RESPONSIBLE FOR THE PROTECLYTIC MATURATION OF THE ALPHA-FACTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROLYL OLIGOPEPTIDASE FAMILY. STRONG, TO DPAP B.
                                                                                                                                                                                                                                                                                                                            931 AA.
                                                                                                                                                                                          624 VRFPNASHNL-SRTGHPRQRIKRLNYISSWF 653
                                                                                                                                                                                                                          733 MWYTDEDHGIASSTAHQHIYTHMSHFIKQCF 763
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=95066382; PubMed=7975897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288C / FY1679;
MEDLINE=96437977; PubMed=8840505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L21944; AAA35119.1; -.
EMBL; U08210; AAA17897.1; -.
EMBL; X92441; CAA63182.1; -.
EMBL; Z75127; CAA99437.1; -.
PIR; A49737; A49737.
PIR; S45451; S45451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flanagan C.A., Thorner J.;
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast 10:801-810(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aminopeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-AB320;
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                                                                                                                                                                                                                                                                                                                     DAP1_YEAST
P33894;
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30;
                                                                        InterPro; IPRU014/1;
Pfam: PF00930; DPPIV_Lerm; 1.
Pfam: PF00930; DPPIV_Lerm; 1.
Pfam: PF00315: Peptidase_S9; IPROSITE; PALSE_NEG.
PROSITE; PS00708; PRO_ENDOPEP_SER; FALSE_NEG.
PROSITE; PS00708; PRO_ENDOPEP_SER; FALSE_NEG.
Transmembrane; Glycoprotein; Signal-anchor; Pheromone response.
DOMAIN 1 19 SIGNAL-ANCHOR (PTPETII MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 DETFEVNLGGNRFLYEGVEFTVSTVQINYKLDKLIFGTNLESEFRHSSKGFYWIKDLNTG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 GSVPWTHGEKRSTD-----PRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 TE---DGSKDIFNAKPDWIYEEEVLASDQAIWWAPDDSK--AVFARFNDTSVDDIRLNRY 389
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
7.7%; Score 269; DB 1; Length 931;
Best Local Similarity 20.1%; Pred. No. 6.4e-10;
Matches 155; Conservative 108; Mismatches 298; Indels 212; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 DSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKEL-TSHKADHGDPAFSPDGKW 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 NIEPILPPEKSDDNYELGLSKLSYAHFSPAYNYIYFVYEN-----NLFLQQVNSGVAKKV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----WSPDGESILVTISLGEGESIDDREKTEQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 TNMNEAYL.SDTKIKYPKPGFQNPQF-DLFLVNLQNGIIYSINTGGQKD----SILYNGKW 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ DLKQVTP-- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    445 ISPDTFRFEI--TDRNSKILDVKVYDIPSSOMLTVRNTNSNLFNGWIEKTKDILSIPPKP 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 --HRGSFGSSSFSPDGRYLALL-------GNEKEYKNATLSKAWLYDIEQG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             503 ELKRMDYGYIDIHADSRGFSHLFYYPTVFAKEPIQLTKGNWEVTGNGIVG----YEYETD 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 RLTCLTEMLDV---HLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTDQGSTGIYYISIE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      559 TIFFTANEIGVMSQHLYSISLTDSTTONTFQSLQNPSDKYDFY--------601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 GLVYPIRLEKEYINSFSLSPDEQHFIASVTKPDRP-----SELYSIPLGQEE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 DITAIVSVTDPQYAPDGTRAAYVKSQVNQEKDS--YTSNI-------WIYETKTG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 KQLTGANDKF---VREHTISIPEEIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648 K----DEKFKEKIKNYDLPITSYKTMYLDDGVEINYIEIKPANLNPKKKYPILVNIYGG 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 PHMMYGHTYF-----HEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGKDYDD 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493 VMQAVDEAIKRD-PHIDPKRLGVTGGSYGGFMTNWIVGQTN--RFKAAVTQRSISNWISF 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           550 HGV-----SDIGYFFTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGER 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              819 DSVYTERYMNQPSENHEGYFEVSTIQNFKSFESLKRLF-------1VHGTF 862
                                                                                                                                                                                                                                              CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                        107200 MW; 81AF70094093C023 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 L---VFSANLTETDDASKPHDVYIMSLESG------
                 SGD; S0005745; STE13.
InterPro; IPR001375; -.
InterPro; IPR002469; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 TDIPYGVSKPL-----
                                                                                                                                                                                                                                                                                                                                       931 AA;
MEROPS; S09.005;
                                                                                                                                                                                                        120
141
785
863
896
377
814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: THE SOLUBLE FORM (SDPP) DERIVES FROM THE MEMBRANE FORM (MDPP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDICINE-91302787; Pubmed-1712807;
MEDICINE-91302787; Pubmed-1712807;
Vivier I., Marguet D.A., Naquet P., Bonicel J., Black D., Li C.X.-Y.,
Vivier I., Marguet D.A., Naquet P., Bonicel J., Black D., Li C.X.-Y.,
Vivier I., Marguet D.A., Naquet P., Pierres M.;

Bernard A.-M., Gorvel J.-P., Pierres M.;

"Evidence that thymocyte-activating molecule is mouse CD26

"Evidence that thymocyte-activating molecule is mouse CD26

"Giopeptidyl peptidase IV).";

J. Immunol. 147:447-454(1991).

- Immunol. 147:447-454(1991).

- PUNCTION: REMOVES N-TERMINAL DIPEPTIDES SEQUENTIALLY FROM
POLYPEPTIDES HAVING UNSUBSCHIUTED N-TERMINI PROVIDED THAT THE
PENULTIMATE RESIDUE IS PROLINE.
                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-GCT-2000 (Rel. 40, Last annotation update)
01-GCT-2000 (Rel. 40, Last annotation update)
MOLECULE) (THYMOCYTE-ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBDUIT: HOMODIMER.
-i- SUBCELLUIAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS IN
A SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY PROTEOLYTIC PROCESSING.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: DIPEPTIDYL-POLYPEPTIDE + H(2)0 = DIPEPTIDE
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "CDNA cloning for mouse thymocyte-activating molecule. A multifunctional ecto-dipeptidyl peptidase IV (CD26) included in subgroup of serine proteases.", J. Biol. Chem. 267:2200-2208(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=B10.A; TISSUE-Liver;
STRAINE=95092780; PubMed=7999781;
BErnard A.-M., Mattel M.-G., Pierres M., Marguet D.;
"Structure of the mouse dipeptidy! peptidase IV (CD26) gene.";
Biochemistry 33:15204-15214(1994).
599 DDRCPIEQAEQLFIALKKMG-KETKLVRFPNASHNLSRTGHPRQRI---KRLNY 648
                                     863 DDNVHIQNTFRLVDQLNLLGLTNYDMHIFPDSDHSIRY--HNAQRIVFQKLYY 913
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=SWISS; TISSUE-Thymus;
MEDLINE-92129288; PubMed=1370813;
Marguet D.A., Bernard A.-M., Vivier I., Darmoul D., Naquet P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marguet D.A.; Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                    760 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U12599; AAA82213.1; JOINED. EMBL; U12600; AAA82213.1; JOINED.
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROLYL OLIGOPEPTIDASE FAMILY.
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                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pierres M.;
                                                                                                                                                        DPP4_MOUSE
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                                                                                                                                     DPP4_MOUSE
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34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 --QGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKWLVFSANL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 VARGDHYLCDVVWATEERISLQWLRRIQNYSVWAICDYD------KINL 329
                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 YNGITDWVYEEEVFGAYSALW------WSPNNTFLAYAQFNDTGVPLIEYSFYSD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 EGGEARKLIDIPYGVSKPLWSPDGESILVTISLGEGESIDDREKTEQDSYEPVEV---- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 145; Conservative 126; Mismatches 281; Indels 178; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KKLITADDI----TAIVSVTDPQYAPDGTRAA-----YVKSQVNQEKDSYTS----NI- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 -----WIYETKTGG--SVPWTHGEKRSTDPRWSPDGRTLAF--ISDREGDAAQLYIMST 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTEWTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 760;
                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                 pfam; PF00930; DPPIV_N_term; 1.
Pfam; PF00326; Peptidase_59; 1.
PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
Hydrolase; Aminopeptidase; Dipeptidase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                  SOLUBLE FORM OF DPP (SDPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A5F644B46E4A3DF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.1%; Score 247; DB 1;
19.9%; Pred. No. 1.3e-08;
                                                           AAA82213.1; JOINED.
AAA82213.1; JOINED.
AAA82213.1; JOINED.
AAA82213.1; JOINED.
AAA82213.1; JOINED.
AAA82213.1; JOINED.
                                                                                                                                                                                  EMBL; U12615; AAA82213.1; JOINED.
EMBL; U12616; AAA82213.1; JOINED.
EMBL; U12617; AAA82213.1; JOINED.
                                                                                                                                                          EMBL; U12613; AAA82213.1; JOINED. EMBL; U12614; AAA82213.1; JOINED.
                                                                                                                                                                                                                             EMBL; U12618; AAA82213.1; JOINED.
EMBL; U12619; AAA82213.1; JOINED
                                                                                                                                                AAA82213.1; JOINED
                                  AAA82213.1; JOINED
                                                  AAA82213.1; JOINED
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                        AAA82213.1;
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InterPro; IPR001375; -
InterPro; IPR002469; -
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679
760 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                          PIR; S23752; S23752
MEROPS; S09.003; -.
                                     U12604;
U12605;
                                                                 U12606;
                                                                                                                                                  U12612;
                                                                                         EMBL; U12608;
                                                                              EMBL; U12607;
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SEQUENCE
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330 TWNCPSEQOHVEMSTIGWVGRFRPAEPHFTSDGSSFYKIISDKDG-YKHICHFPKDKKDC 388
                                266 TL--SKAWLYDIEQGRLTCLTEMLDVHLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTD 323
                                                                                                    324 QGSTGIYYISIE-----GLVYPIRLEKEYIN----SFSLSPDE-QHFIASVTK---- 366
                                                                                                                                 410 -----YISNOYKEMPGGRNLYKIQL-TDHTNVKCLSCDLNPERCOYYAVSFSKEAKYY 462
                                                                                                                                                                      367 -----PDRPSELYSIPLGQEEKQLTGANDKFVREHTISIPEEIQYATE--DGVMVNG-- 416
                                                                                                                                                                                                       463 QLGCWGPGLP--LYTLHRSTDHKELRVLEDNSALDRML---QDVQMPSKKLDFIVLNETR 517
                                                                                                                                                                                                                                       417 -W--LMRPAQMEGETTYPLILNIHGGPHMMYGHTYFH----EFQVLAAKGYAVVXINPRGS 470
                                                                                                                                                                                                                                                             471 HGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWIVGQ 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                               588 ETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNL-SRTGHPRORIKRL 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-89123496; PubMed-2563382;
Ogata S., Misumi Y., Ikehara Y.;
"Primary structure of rat liver dipeptidyl peptidase IV deduced from its cDNA and identification of the NH2-terminal signal sequence as the membrane-anchoring domain.";
J. Blol. Chem. 264:3596-3601(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (GP110 GLYCOPROTEIN)
(BILE CANALICULUS DOMAIN-SPECIFIC MEMBRANE GLYCOPROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hong W., Doyle D.; "Molecular dissection of the NH2-terminal signal/anchor sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hong W , Doyle D , "CDNA cloning for a bile canaliculus domain-specific membrane
                                                                 389 TFITKGAW-------EVISI---EALTSDYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein of rat hepatocytes.";
Proc. Natl. Acad. Sci. U.S.A. 84:7962-7966(1987)
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MEDLINE-88068516; PubMed=3479775;
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J. Cell Biol. 111:323-328(1990).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                               PTM: THE SOLUBLE FORM (SDPP) DERIVES FROM THE MEMBRANE FORM (MDPP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                Iwaki-Egawa S., Watanabe Y., Fujimoto Y.;
"N-terminal amino acid sequence of the 60-kDa protein of rat kidney
dipeptidyl peptidase IV.";
Biol. Chem. Hoppe-Sevler 374:973-975/1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 SISDYSVSPDRLEVLLEYNYVKQWRHSYTASYSIYDLNKRQLITEEKIPNNTQWI---- 153
                                                                                                                                     -!- CATALYTIC ACTIVITY: DIPEPTIDYL-POLYPEPTIDE + H(2)0 = DIPEPTIDE
                                                                                                                                                                                    SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS IN A SOLUBLE FORM.
                                                                                                                                                                                                                              BY PROTEOLYTIC PROCESSING.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
PROLYL OLIGOPEPTIDASE FAMILY.
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                                                                                       FUNCTION: REMOVES N-TERMINAL DIPEPTIDES SEQUENTIALLY FROM POLYPEPTIDES HAVING UNSUBSTITUTED N-TERMINI PROVIDED THAT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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Pfam; PF00330; DPDIV_N_term; 1.

Pfam; PF00336; PPDIV_SOURCES, 1.

PROSITE; PS00708; PRO_ENNOPEP_SER; 1.

Hydrolase; Aminopeptidase; Dipeptidase; Serine protease; Transmembrane; Glycoprotein; Signal-anchor.

CHAIN 1 767 MEMBRANE FORM OF DPP (MDPP).
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60 KDA SOLUBLE FORM OF DPP.
CYTOPLASMIC (POTENTIAL).
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I -> T (IN REF. 2)

C -> V (IN REF. 2)

V -> D (IN REF. 2)

L -> F (IN REF. 2)

L -> F (IN REF. 2)

R -> Q (IN REP. 2)

AA17C0BC6F0E4652 CRC64;
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N-LINKED (GLCNAC...)
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18.2%; Pred. No. 2.5e-08;
                                                                             Hoppe-Seyler 374:973-975(1993)
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7.0%; Score 242.5; Best Local Similarity 18.2%; Pred. No. 2.5e-Matches 134; Conservative 122; Mismatches
                                                                                                                         IS PROLINE.
            MEDLINE=94128239; PubMed=7905271;
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686
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352
394
562
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767 AA;
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#EDLINE=92108018; PubMed=1729689; Wada K., Wenthold R.J., Shimasaki S.; Wada K., Yokotani N., Hunter C., Doi K., Wenthold R.J., Shimasaki S.; "Differential expression of two distinct forms of mRNA encoding members of a dipeptidyl aminopeptidase family."; Proc. Natl. Acad. Sci. U.S.A. 89:197-201(1992).
-:- FUNCTION: MAX BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                       167 AYAQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSL 226
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                                                                                                                                                                                                                                      227 ESGDLKQVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSKAWLYDIEQGRLTCL--- 283
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                                                                                                                                                                                                                                                                                                                                                       329 DKTTLVWNCPTTQEHIETSATGWCGRFRPAEPHFTSDGSSFYKIVSDKDGYKHICQFQKD 388
                                                                        109 -YGVSKPL-WSPDGESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRG 166
                                154 ----TWSQEGHKLAYVWKND-----IYVKIEPHLPSHRITSTGKENVIFNGINDWVYEEE 204
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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DIPEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
RELATED PROTEIN) (DIPEPTIDYLEPTIDASE VI) (DPPX).
66 STDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIP-
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TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASLYORFTGKINTSRSFPAPPEASHLLGGQGPEEDAGSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGPQAQAVAPRERGGAGGRPRFQYQARSDCDEED -> MTT
AKEPSASGKSVQQQDQ (IN ISOFORM DPPX-S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 QVTPHRGSFGSSSFSPDGRYLALLGNEKEYKNATLSK---AWLYDIEQGRLTCLTEMLDV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 HLADALIG-----DSLIGGAEQRPIWTKDSQGFYVI-GTDQGSTG-IYYISI--- 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 -LCDATTGVCTKKHEDESEAWLHRONEEPVFSKDGRKFFFVRAIPOGGRGKFYHITVSSS 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 GPKGQQLIFIFEN----NIYYCAHVGKQAIRVVSTGKEGVIYNGLSDWLYEEEILKSHI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 ---WSPDGESILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 AHWWSPDGTRLAYA------TINDSRVPL-------MELPTYTGSV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 LVSVKSGEMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSLESGDLK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 YPTVKPYHYP----KAGSENPSISLH----VIGLN-----GPTHDLEMMPPDDPRMR 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 SPDGRTLAFISDREGDAQLYIMSTEGGEARKLTD-----IPYGVSKPL------ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 IRYEISPDKEYALFSYNVEPVYQHSHTGYYVLSKIP--HGDPQSLDPPEVSNAKLQYAGW 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 104; Mismatches 246; Indels 242; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 VKSQVNQEKD----SYTSNIWIYETKTG----GSVPWTHGEKRSTDP-----RW 71
FUNCTION. HAS NO DIPPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE FOR THE SERINE RESIDUE IN THE PROPOSED CATALITIC TRIAD.

SUBSCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).

SUBSCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).

ALTERNATIVE PRODUCTS: 2 ISOFORMS: DPPX-L (SHOWN HERE) AND DPPX-S; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECTFICITY: DPPX-S IS EXPRESSED IN BRAIN AND SOME PERIPHERAL TISSUES PRODUCK KINDING KIDNEY, OVARY, AND TESTIS; IN CONTRACT DPPX-I IS EXPRESSED ALMOST EXCLUSIVELY IN BRAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSTRICT PROPOSAGE DEPLY_Lerm; 1.
Pfam; PF00326; Peptidase_S9; 1.
Transmembrane; Glycoprotein; Signal-anchor; Alternative splicing.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.7%; Score 233; DB 1; Length 859; Similarity 19.9%; Pred. No. 1.2e-07;
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                                                                                                                                                                                                      PROLYL OLIGOPEPTIDASE FAMILY.
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5B 1 GPNSSNDNIQSITSGDWDVTE	3/3 SIPL	410 DGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFHEF 452 	51	ISNWISEHGV	53	- H		RESULT 11  DPP6_HUMAN  TD DPP6_HUMAN  STANDARD; PRT; 865 AA.  P42658;  DT 01-NOV-1995 (Rel. 32, Created)  DT 01-NOV-1995 (Rel. 32, Last sequence update)  DT 01-OCT-2000 (Rel. 40, Last annotation update)  DE DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-	Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9666;	A. us; ; PubMed=: K., Went] n of a cai	In encoded by a		THE SERING RESIDUE IN THE PROPOSED CATALYTIC TRIAD. ELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBBLE). RNATIVE PRODUCTS: 2 ISOPORMS: DPPX-1, (SHOWN HERE) AND	AIN.	NOLID OLIGOPEPTIDASE FAMILY.	borat tatio	profit institutions as long this statement is not removed	reydines a license agreement (See http://www.isb-sib.ch an email to license@lsb-sib.ch).
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EMBL; M96859; AAA35760.1; -.

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40;
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N-LINKED (GLCNAC...) (POTENTIAL).
MASLYOFFTGKINTSRSFPAPPEASHLLGGGGFEDGGAGA.
                                                                                                  Signal-anchor; Alternative splicing.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TVPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                            KPLGPRAQAAAPRERGGGGGGGGGGRPRFQYQGRSDGDED
-> MTTAKEPSASGKSVQQOEOE (IN ISOFORM DPPX-
                                                                                                                                                                                                                                                                                                                                                                            6.4%; Score 224; DB 1; Length 865;
conservative 117; Mismatches 263; Indels 274; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 KKKVTVEDLFSEDFKIHDPE-----AKWISDTEFIYREOKGTVRLWNVETNT--STVL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 THGEK----RSTDPRWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 IEGKKIESLRAIRYEISPDREYALFSYNVE----PIYQHSYTGYYV--LSKIPHGDPQSL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 --------WSPDGESILVTISLGEGESIDDREKTEQDSYEPVEV--QGLSYKRD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 DPPEVSNAKLQYAGWGPKGQQLIFIF-----ENNIYYCAHVGKQAIRVVST 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 GK-----GLTRGAYAQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKWLVFSANLTETD 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 DASKPHDVYIMSLE--SGDL-KQVTP-HRGSFGSSSFSPDGRYLALLG------ 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 -NEKEY-----KNATLSK---AWLYDIEQGRLTCLTEMLDVHLADALIG------D 298
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKLITADDI-TAIVSVTDPQYAPDGTRAAYVK-SQVNQEKDSYTSNIWIYETKTGGSVPW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428 AWLHRQNEEPVFSKDGRKFFFIRAIPQGGRGKFYHITVSSSQPNSSNDNIQSITSGDWDV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 --VIGTDQGSTGIYYISIEGL-----VYPIRLEKEYIN------SFSLSP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 D--FFLLKCEGPGVPMVTVHNTTDKKKMFDLETNEHVKK--AINDR-----QMPKVEY 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405 QYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGGPHMMYGHTYFHEFQV-----LAAK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 RDIEIDDYNLPMQILKPATFTDTTHYPLLLVVDGTPG---SQSVAEKFEVSWETVMVSSH 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 GYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVMQAVDEAIKRDPHIDPKRLGVTGGS 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 DEQHFIASVTKPDRP-----SELYSIPLGQEEKQLTGANDKFVREHTISIPE-EI 404
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                                                                                                                                                                                                                                                                                                                                    14BlAE0E0024464B CRC64;
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                                    InterPro; IPR001375; -.
InterPro; IPR001375; -.
InterPro; IPR002469; -.
Pfam; Pr003026; Deptv_Nterm; 1.
Pfam; Pr00326; Peptidase_$9; 1.
Transmembrane; Glycoprotein; Sig
                                                                                                                                                                                                                                                                                                                                    865 AA; 97588 MW;
EMBL; M96860; AAA35761.1;
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173
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                809.973;
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                           MIM; 126141;
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               MEROPS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDLINE-94378003; PubMed-8091229;
MEDLINE-94378003; PubMed-8091229;
MEDLINE-94378003; PubMed-8091229;
Johnston M., Andrews S., Brinkman R., Geisel C., Kirsten J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Jöhnston L., Langston Y.,
Latrellle P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                              559 FTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMG 618
                                                                                                                    769 MT--KVAH-----RVSALEBQQFLIIHPTADEKIHFQHTAELITQLIRGK 811
519 YGGFMINWIV------GQT-----GAT-----568
                                   713 YGGYLSTYILPAKGENQGQTFTCGSALSPITDFKLYASAFSER----YLGLHGLDNRAYE 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLYL OLIGOPEPTIDASE FAMILY. STRONG, TO DPAP A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 265:2077-2082(1994).
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. LYSOSOME-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roberts C.J., Pohling S. Rothman J.H., Stevens T.H.;
"Structure, biosynthesis, and localization of dipeptidyl
aminopeptidase B, an integral membrane glycoprotein of the yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Fungi; Ascomycota: Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
DIPEPTIDYL AMINOPEPTIDASE B (EC 3.4.14..) (DPAP B) (YSCV).
                                                                                                                                                                619 KETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                                                                                      812 ANYSLQIYPDESH-----YFTSSSLKQHL 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell Biol. 108:1363-1373(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89174971; PubMed=2647766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00930; DPPIV_N_term; 1. Pfam; PF00326; Peptidase_S9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X15484; CAA33512.1; -.
EMBL; U10399; AAB68879.1; -.
PIR; A30107; A30107.
PIR; S46780; S46780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD; S0001070; DAP2.
InterPro; IPR001375; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002469; -.
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DAP2 OR YHR028C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                               DAP2_YEAST
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35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 AKGYA-VVYINPRGSHGYGQEFVNAVR---GDYGGKDYDDVMQAVDEAIKRDPHIDPKRL 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                618 SOLNAIVVVVDGRGTGFKGQDFRSLVRDRLGDYEARDQISAASLYGSL----TFVDPQKI 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              513 GVTGGSYGGFWTNWIVGOT--NRFKAAVTORSISNWISFHGVSDIGYFFT----DWOLE 565
                                                                                                                                                                                                                                                                                                                                  AKRAFDGQFVK -> QSVLSMGNLTNELTIYSSSHKDIHKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 -----ILVNSYEILPNDFD-ETLSDHYPVFFFAYGGPNSQQVVKTFSVGFNEVVA 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 QGST--GIYYISIEG---LVYPIRLEKEYINSFSLSPDEQHFIASVTKPDRP----- 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456 KSSTERHVYIDLRSPNEIIEVIDTSEDGYYDVSFSSGRRFGLLTYKGPKVPYOKIVDFH 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 -----SELYSIPLGQEEKQLTGANDKFVREHTISIP 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 NATLSKAWLYDIEQGRLTCLTEMLDVHLADALIGDSLIGGAEQRPIWTKDSQGFYVIGTD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427 TLTEGK---WEVVNGPLAF-----LYFISTR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 SILVTISLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 KELTSHKADHGDPAFSPDGKWLVFSAN-----LTETDDAS------KPHDV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 --TSFHPRISGN---KKDGSLLITEVTWVGNGNVLVKTTDRSSDILTVFLIDTIAKTSNV 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 YIMSLESGDLKQVT-----GNEKEYK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 VRNESSNGGWWEITHNTLFIPANETFDRPHNGYV---DILPIGGYNHLAYFENSNSSHYK 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 VFEDDKAAWWSPTGDYLAFLKIDESEVGEFI-----IPYIV----- 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 ------TPNPHAELWVYSMKDG-- 314
194 WSPNSNDIAYVQD-----NNIYIYSAISKKTIRAVTNDGSSFLFNGKPDWVYEEE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 RSTDPR---WSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTDIPYGVSKPLWSPDGE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                              98; Mismatches 239; Indels 247; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 YAPDGTRAAYVKSQVNQEKDSYTSNIWIYET---KT------GGSVPWTHGEK 64
                                                                                                                           N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                     TSNVVRNESS -> DFKRGKERKF (IN REF. 1)
                                                                   LUMENAL (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 818;
                                                                                                                                                                                                                                                                                    FEEIGNE -> LRRLET (IN REF. 1).
D -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                          SYLHUMXI (IN REF. 1).
318F450445375BD3 CRC64;
                                                                                                                                                                                                                                                               O -> H (IN REF. 1).
S -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                  6.3%; Score 218.5; DB 1
19.9%; Pred. No. 9.9e-07;
                                                                                                                                                                                                                                                                                                                                                        FSYLHTMYI (IN REF.
                                                                                                                                                                                                                                                                                                                                                                            818 AA; 93404 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 145; Conservative
                                                                                                                                                                                                                  3392
421
738
83
125
125
200
200
818
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                                                                                                                              SITE
                                                                 PRANSMEM
                                                                                               ACT_SITE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      674 SLFGWSYGGYLTLKTLEKDGGRHFKYGMSVAPVTDWRFYDSVYTERYMHTPQENFDGYVE 733
                            566 HDMFEDTEKLWDRSPLKYAANVETPLLILHGERDDRCPIEQAEQLFIALKKMGKETKLVR 625
                                                   734 SSVHNVT-----ALAQANRFLLMHGTGDDNVHFQNSLKFLDLLDLNGVENYDVH 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IS EXPRESSED EXCLUSIVELY IN THE BRAIN WHEREAS DPPX-S IS FOUND IN BRAIN, KIDNEY, OVARY AND TESTIS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN. DPPX-L
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
DIPEPTIDXL PEPTIDXE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-RELATED PROTEIN) (DIPEPTIDXEDETIDXEDETIDXEDETIDXEDETIDXEDETIDXEDETID
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                    863 AA
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92108018; PubMed=1729689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROLYL OLIGOPEPTIDASE FAMILY.
                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M76428; AAC41622.1; -. EMBL; M76429; AAC41623.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00930; DPPIV_N_term;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fransmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00326; Peptidase_S9;
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001375; -. InterPro; IPR002469; -.
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171
402
469
533
564
811
                                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114
                                                                                                                                                                                                                                                                                                taurus (Bovine)
                                                                                                             783 VFPDSDHSI 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S09.973;
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
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402
469
533
564
811
                                                                                  - FPNASHNL
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                 DPP6_BOVIN
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MASLYQRFTGKINTSRSFPAPPEASRLLGGQGPEEDGAGPK
PLGAQAPAAAPRERGGGGGGAGGRPRFQYQARSDCDDED ->
                                                                                                                                                                                                                                              183 ESLRAIRYEISPDREYALFSYNVEPIYQHSYTGYYVLSKIP--HGDPQSLDPPEVSNAKL 240
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                        70 ----RWSPDGRTLAFISDREGDAAQLYIMSTEGGEARKLTD-----IPYGVSKPL---- 115
                                                                                                                                                                                                                                                                                                                  241 QYAGWGPKGQQLIFIFEN-----NIYYCAHVGKQAIRVVSTGKEGVIYNGLSDWLYEEEI 295
                                                                                                                                                                                                                                                                                                                                                                        313 YATINDSRVPWMELPTYTGSVYPTAKPYHYPKAGCENPSISLHVIGLNGPTHDL----- 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 SGDLKQVTPHRGSFGSSSFSPDGRYLALLGNEKEY----KNATLSKA---WLYDIEQGR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 -----EMTP-------PDDPRM------REYITHWKWATSTKVAVNWLSRAQ--N 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 LTCLTEMLDVHLADALIG----- 318
                                             MTTAKEPNASGKSVQQQEQ (IN ISOFORM DPPX-S).
23DBA792B841A39D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 YAQLVLVSVKSGEMKELTSHKADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSLE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  403 VSILT-----LCDATTGVCTKKHEDESEAWLHRONEEPVFSKDGRKFFFVRAIPQGGQG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SLSPDEQHFIASVTKPDRPSELYSIPLGQEEKQLT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GANDKFVREH---TIS---IPE-EIQYATEDGVMVNGWLMRPAQMEGETTYPLILNIHGG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440 PHMM----YGHTYFHEFQVLAAKGYAVVYINPRGSHGYGQEFVNAVRGDYGGKDYDDVM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----- 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 KFYHITVSSSQPNSSNDNIQSITSGDWDVTKILSYDEKRSQIYFLSTEDL--PRRRQLYS 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAVRVMLK-EPYIDKTRVAVFGKDYGGYLSTYLLPAKGDGQAPVFSCGSALSPITDFKLY 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747 ASAFSERYLGLHGLDNRAYEMA--KVAH-------RVSALEGQQFLVIHATA 789
                                                                                                                                                                                                       24 DGTRAAYVKSQVNQEKDSYTSNIW-IYE-TKTG----GSVPWTHGEKRSTDP----- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           599 DDRCPIEQAEQLFIALKKMGKETKLVRFPNASHNLSRTGHPRQRIKRLNYISSWFDQHL 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SAALQQHL 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    515 ASTVGSFNRQCLSCDLVDNCTYFSASFSPGADFFLLKCEGPGVPT--VSVHNTTDKKKMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 573 --- DLETNEHVQKAISDRQMPKVEYRKIETDDYNLPIQILKPAIFTDTAHYPLLLVVDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----WISFHGVSDIGYFFTDWQLEHDMFEDTEKLWDRSPLKYAANVETPLLILHGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495 QAVDEAIKRDPHIDPKRLGVTGGSYGGFMTNWIV----GQTNRFKAAVTQRSISN----
                                                                                                                                                                    249; Indels 273;
                                                                                                                       Ouery Match 6.1%; Score 211.5; DB 1; Length 863; Best Local Similarity 19.5%; Pred. No. 3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOLB_HAEIN STANDARD, PRT; 427 AA. P44677; P94811; 01-NOV-1995 (Rel. 32, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEKIHFOHTAELITQLIKGKANYSLQIYPDESHYFS ----
                                                                                                                                                              Matches 152; Conservative 105; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 296 LKTHIAHWWSPDG------
                                                              96556 MW;
  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOLB PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae
                                                            863 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOLB OR HI0382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 KEYINSF-
                                                            SEQUENCE
                                                                                                                         Query Match
  VARSPLIC
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 SLGEGESIDDREKTEQDSYEPVEVQGLSYKRDGKGLTRGAYAQLVLVSVKSGEMKELTSH 187
                                                                        MEDLINE=95350630; PubMed=7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soct J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Witerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                      MEDILINE=97080550; PubMed=8921895;
Sen K., Sikkema D.J., Murphy T.F.;
Sen K., Sikkema D.J., Murphy T.F.;
Isolation and characterization of the Haemophilus influenzae tolQ,
tolR, tolA and tolB genes.";
Gene 178:75-81(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 SPAWSPDGQRLAYVS-FENKKSQLVVQDLNSGARKVVASFQGHNGAPAFSPDGSRLAFAS
                                                                                                                                                                                                                                                                                                                                                                                                                   -i - FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102; Indels 114;
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mhole-genome random sequencing and assembly of Haemophilus influenzae \operatorname{Rd}. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.4%; Score 190; DB 1; Length 427;
24.4%; Pred. No. 2.8e-05;
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STRAIN 1479).

STRAIN 1479).

STRAIN 1479).

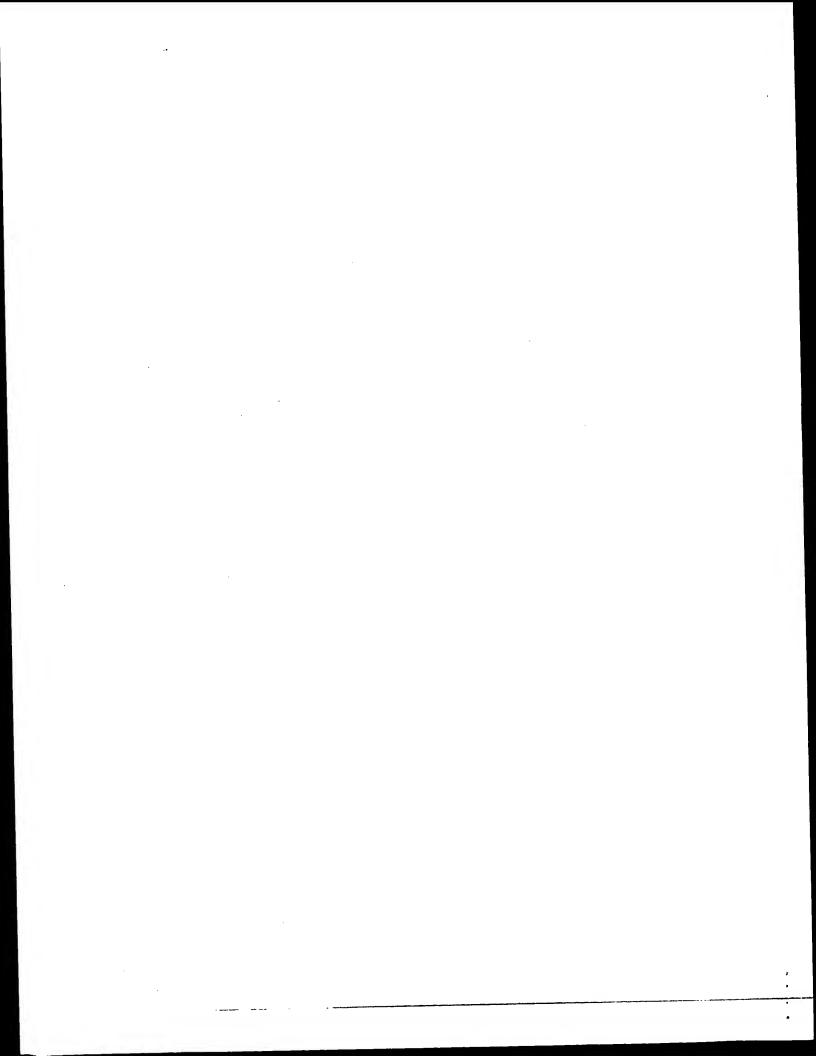
STRAIN 1479).

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V -> I (IN STRAIN 1479).
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                                                                                                                                                                                                                                                                              Science 269:496-512(1995).
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Matches 80; Conserv
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                              NCBI_TaxID=727;
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                   Haemophilus
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339 ADGKTLVMINGNNNVVKODLTTGVSEVLSTSFLGESPSLSPNGIMIIYSSTQG----LGK 394
                                                                                        289 AGNNTEPAWSPDGNSILF-----TSDRSGSPQVYRMDASGGSATAV----GGRGSAQIS 338
                                                                                                                              ----YDIEQGRLTCLTE 285
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Biochem. J. 276:837-840(1991).
-!- FUNCTION: CLEAVES PEPTIDE BONDS ON THE C-TERMINAL SIDE OF PROLYL.
RESIDDES WITHIN PEPTIDES THAT ARE UP TO APPROXIMATELY 30 AMINO
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-!- TISSUE SPECIFICITY: IN ALL TISSUES.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9A; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROLYL ENDOPEPTIDASE (EC 3.4.21.26) (POST-PROLINE CLEAVING ENZYME)
                                                   188 KADHGDPAFSPDGKWLVFSANLTETDDASKPHDVYIMSLESGDLKQVTPHRGSFGSSSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVE SITE HIS-680.
MEDLINE-91291146; PubMed=2064618;
Stone S.K., Rennex D., Wikstrom P., Shaw E., Hofsteenge J.;
Stone S.K., Rennex D., Wikstrom P., Shaw E., Hofsteenge J.;
Inactivation of prolyl endopeptidase by a peptidylchloromethane.
Kinetics of inactivation and identification of sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rennex D., Hemmings B.A., Hofsteenge J., Stone S.R.; "cDNA cloning of porcine brain prolyl endopeptidase and identification of the active-site seryl residue."; Biochemistry 30:2195-2203(1991).
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(Rel. 20, Last sequence update)
(Rel. 33, Last annotation update)
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80769 MW;
Hydrolase; Serine protease.
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44: em_ov:* 45: em_pat:* 46: em_pat:* 48: em_rbi:* 49: em_rbi:* 49: em_xi:* 51: em_vi:* 52: em_vi:* 53: qb_sts:* 54: qb_sts:* 55: qb_vi:* 56: qb_by:* 60: qb_htg1:* 60: qb_htg1:* 61: qb_htg2:* 62: qb_htg3:* 63: qb_htg1:* 64: qb_htg1:* 65: qb_htg1:* 66: qb_htg1:* 67: qb_htg1:* 68: qb_htg1:* 69: qb_htg1:* 71: qb_htg1:* 72: qb_htg1:* 73: qb_htg1:* 74: qb_htg1:* 74: qb_htg1:* 75: qb_htg1:* 76: qb_htg1:* 77: qb_htg1:* 78: qb_htg1:* 78: qb_htg2:* 79: qb	No. is the number of results predicted by chance to have
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SUMMARIES

Description	HOTO AT TORSO	し にたじりひひゃん	Avodoki Sequence	ATTAGOR S	AUZ48Z88 Pyrococcu	AAU41922 Sequence	POOCOCCUS	APOUNDS Pyrococu	AP000062 Aeropyrum	
ID		AX006271	BSUB0017	CNSPAXOR	AX041922	E16634	AP000003	AE001879	AP000062	
DB	1	6	7	~	0	10		-	7	
Query Match Length DB ID		1971	217420	265118	265118	1896	233000	9.7 10256	251700	
Query Match		100.0	100.0	12.1	12.1	11.5	11.5	9.7	8.2	
Score		1971	1971	238.2	238.2	227.2	227.2	191.2	161.8	
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AE005872 Caulobact
AC090315 Homo sapi
AC025602 Homo sapi
AC010044 Drosophil
U13070 Caenorhabdi
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AL512970 Sulfolobu
AL445065 Thermopla
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AE004038 Xylella f
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AF059278 Entamoeba
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                                                  AP000064 Aeropyrum
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                                   AP000993 T
AE005114 F
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AR095647
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                                                                                                                                                                                                                                                                                                                                                                                                                  Proteases from gram-positive organisms
Patent: WO 9903984-A 1 28-JAN-1999;
GENENCOR INVERNATIONAL B V (NL); ESTELL DAVID A (US)
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Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 to 1971)
Estell,D.A.
                                                                                                                                                                                                                                                                                                                                   PAT
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/db_xref="taxon:1423"
431 c 524 g 458 t
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Best Local Similarity 100.C
Matches 1971; Conservative
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Bacillus subtilis
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67965
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136257
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ORIGIN
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              togtatacatoaaatatatggatotatgaaacgaaaacgggaggatotgttoottggaca 180
                  gtttacataatgtcactggagtctggagtcttaagcaggttacacctcatcgcggctca
                                             gcaagaaaactgactgatatcccatatggcgtgtcaaagccgctatggtccccggacggt
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Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.
1141 gaagagaaacagctgactggcgcgaatgacaagtttgtcagggagcatacgatatcaata 1200
             cctgcacaaatggaaggtgagacaacatatccacttattcttaacatacacggcggtccg 1320
                                                                                                      1321 catatgatgtacggacatacatattttcatgagtttcaggtgctggcggcgaaggatac 1380
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Azevedo,V., Bertero,M.G., Bessieres,P., Bolotin,A., Borchert,S.,
Borriss,R., Boursier,L., Brans,A., Braun,M., Brignell,S.C.,
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Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Enriantoch, E.D., Enrington, J., Fabrer, C., Errarich, S.D., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fabrer, C., Ferrari, E., Galleron, N., Ghim, S.Y., Glasor, P. Golfeau, A., Golightly, E.J., Henaut, G., Guiseppi, G., Guy, B.J., Haga, K., Halech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hullo, M.F., Italio, M.F., Kalaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Konligsteln, G., Krogh, S., Kamano, M., Kurita, K., Lapidus, A., Lavino, S., Mauel, C., Kobayashi, Y., Koetter, P., Masuda, S., Mauel, C., Madi, S., Noback, M., Noone, D., O'Keilly, M., Portetelle, S., Mauel, C., Madi, S., Noback, M., Noone, D., O'Keilly, M., Portetelle, D., Porvollik, S., Prescott, A.M., Prescoan, E., Pujic, P., Rurolla, C., Rocha, E., Roche, B., Rose, M., Sadale, Y., Sato, T., Sckowska, A., Seror, S., Schroeter, R., Soldo, B., Schoeler, R., Soldo, B., Sorokin, A., Tacconi, E., Taragi, T., Takahashi, H., Takemaru, K., Tosato, V., Uchiyama, S., Vandenbol, M., Vannier, P., Tognoni, A., Vari, A., Wambutt, R., Wambutt, R., Wambutt, R., Wambanoto, H., Vamane, K., Yasumoto, K., Yata, K., Danchin, A., Tanka, H., Takama, H., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (18-Nov-1997) I. Moszer, A. Danchin, Institut Pasteur,
Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724
Paris Cedex 15, FRANCE. E-mail: moszerépasteur.fr,
adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
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AVERDELKPQHFENWVKWAKNLGLGLDFNPTLFSHEKAADGLTLSHPDPDIREFWIRH
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LYTDKLALHVSRPVRWDSDHVVVLDDELREIALEIVRNHALEKVALGLDFEDASINRV
AAWTIGTRNMIKALLYALLLPNGYLKQLQEEGRYTERLALMEEFKTYPPGAIWDSYCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The complete genome sequence of the gram-positive bacterium Bacillus subtilis
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/db_xref="taxon:1423"
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/gene="yulf"
/function="unknown"
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/gene="yulf"
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SHCMIDSKHPRREIETLHAFLPYKHYDHTHPDAIISICCADNGKQIAEDIYGNRFWW
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GQFVSLHENESYHVEXWPLELYKLILAPPEAEFSRKYALITGGAGGIGSAACRRFAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGHVIVADLNIEGAQKIAGEINDAYGKGRAMAYKMDYTKEEDVQSAFERAALAYGGID
IVVNNAGLATSSPFDETSLKEWNLNMNVLGTGYFLVAREAFKQMKHQNRGGSWYFVGS
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ETYHVMKTELSCKEFOVHUGNSDSNEWQALLKKRMIERSDGTILMADSSKWGNREFSH
IASLQDVSRLITDSGLDPASVKALEDKKVVTAVPLSKRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EERAAAYGIEPDQLEEHYRKRTALLVNIYPEDIAEAIAFFASSKAEKTTGCMITVDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MVKHIWDSERAAQLPKGVEELVYRSNLIGSDRTVCNWGGGNTSM
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                                                                                complement(1635. .3092)
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RGFSVVAEPVRKLAVQSABSAKEIEGLIQEIVREISTSLSMFQSVNHEVKBGLQITDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DROMMGSALENVOOLNEIINTSIGEKENSADYFSEWLTKEKYNAKSNASIREKFSOYI
SINKDVESIYISDIKGHFIRYPDLPMPSGYNEVERDMYKKAVANKGKVVIIDPYKTAS
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                                                                                         /translation="MGKFIQWIKQPSISKPLIAAFLAVLILPVGVLAYFSYQSAWNAL
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TLNDDVGAIYAASEDKKLYKYPDSGVPKGFDPTGRDWYKQAVAEKGQAVFSEPYTDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD 114674 ICGIATACAICAAATATAIGGAFCTAIGAAACGAAAACGAAAACGAAACGAATCTGTAGACA 114615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="chemotaxis deficiency toward glucose and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="methyl-accepting chemotaxis protein"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1971; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       complement(8204. .10224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(8239. .10224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(8204. .8228)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha-methyl-glucoside"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="mcpA"
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EVRVNIEKARARGWVDERAIVEFSKFRAYVAWKFDKYVDFWATFEDEPMYTAELGYLAP
                                                                                                                                                                                                             DD 113114 GACTGCCAGCTTGAGCATGACATGTTTGAGGACACAGAAAAGCTCTGGGACCGGTCTCT 113055
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                                                                                                                                                                                                                                                                                 Db 113054 TTAAAATACGCAGCAAACGTGGAGACACCGCTTTTGATACTGCATGGCGACGGGATGAC 112995
                                                                                                                                                                                                                                                                                                                                                        Db 112994 CGATGCCCGATGGAGCAGCGGAGCAGCTGTTTATCGCTCTGAAAAAAATGGGCAAGGAA 112935
                                                                                                                                                                                                                                                                                                                                                                                                         1681 gactggcagcttgagcatgacatgtttgaggacacagaaaagctctgggaccggtctcct 1740
                                                                                                                                                                                                                                                                1741 ttaaaatacgcaagcaaacgtggagacaccgcttttgatactgcatggcgagcgggatgac 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
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Genoscope.
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164. 1615
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KVY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVTEVYSIANEGSOKGDEALKRIEDIOHMMSRIEETVSKVAEMSRNIEEITNVITSIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LELYGIWDRVPESVRSHIEKGIRGEAEFILKEELPNIHNFLIASNSISCOAVVEEATK
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Anote-"PAB1338"
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COMPLEMEN (13717. . . 14823)
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Matches 495; Conservative
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Forterre, P., Thierry, J.C., Prieur, D., Dietrich, J., Lecompte, O., Querellou, J., Welssenbach, J., Saurin, W., Heilig, R., Flament, D., Raffin, J. P., Henneke, G., Guequen, Y. and Rolland, J.L., Genome sequence and polypeptides of pyrococcus _i(abissy), fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and uses thereof
Patent: WO 0065062-A 817 02-NOV-2000;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (FR) ; IFREMER
INSTITUT FRANCAIS DE RECHERCHE POUR L'EXPLOITATI; ON DE LA MER (FR)
Db 58070 ATTCCCAGGTGAGAATCATGACTTGAGTAGGAGTGGAAGGCTTAAGAG 58011
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                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                    AX041922 265118 bp DNA
Sequence 817 from Patent WO0065062.
                                                                                               58010 GCTCGAGCTCATAGTGGGGTGGTTTGA 57984
                                                          1935 cctgaattatatcagctcatggtttga 1961
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C12N15/09,C07H21/04,C12N9/78,C12Q1/37,(C12N15/09,C12R1:01), PC
                                                                                                                                                                                                                                                                 58130 cGAGGCTTTGCAATTTTACATAGCGTTGAAGTATTTGGGCAAAACCGTCGAGCTGGCGAT 58071
                                                                                                                                                                                                                                                                                                                                                                           58070 ATTCCCAGGTGAGAATCATGACTTGAGTAGGAGGTGGAAGGCCAAAGCATAGGGTTAAGAG 58011
                                                                                         1875 ttttccgaatgcatcgcacaatttatcacgcaccggacacccaagacagcggatcaagcg 1934
                                                     58430 CTTATAGATGAGGAAAGGCTTGGCGTTACCGGAGGATCATACGGAGGCTTCATGACAAA 58371
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AGENCY OF IND SCIENCE & TECHNOL
1695 gcatgacatgittgaggacacagaaaagcictgggaccggictcoittaaaatacgcagc 1754
                                                                                                                                                                                                                                                 1635 ttggatcagctttcacggcgtcagtgatatcggctatttctttacagactggcagcttga 1694
                                        product='aminoacylase/carboxypeptidase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E16634 1896 bp DNA PAT 28-JUL-199
Pyrococcus horikoshi gene for aminoacylase/carboxypeptidase.
B116634
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31-JAN-1997 JP 1997018381
ISHIKAWA KAZUHIKO, MATSUI IKUO, ISHIDA HIROYASU, PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                    58010 GCTCGAGCTCATAGTGGGGTGGTTTGA 57984
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BCT 06-APR-2000 Py DNA BCT 06-APR-2000 Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt. position (3/7).
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ABO09490 ABO09491 ABO09492 ABO09493 ABO09494 BAO00001
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                                                                                                                                                                              1061 ATGGAAAGGAGAAGGTTACCGACTTTAACAAATGGATAAAGGGTTACACCCTTTCAA 1120
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                                                                              DB 10; Length 1896;
                                                                               Query Match
11.5%; Score 227.2; DB 10; Length
Best Local Similarity 55.4%; Pred. No. 7.5e-60;
Matches 461; Conservative 0; Mismatches 368; Indels
/db_xref="taxon:32644"
358 c 491 g
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/note="similar to Swiss_Prot:P30665 percent
identity:41.538 in 331aa. motif=ATP/GTP-binding site motif
A (P-loop); protein splicing signature"
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MVKEVGAEHINKLIQVEGVVTRVTEIKPFVSVAVFVCKDGHEMVVPQKPYEGFVAVK
KCEQCGSKNYQLDVEKSKFVNFOMFRIODRPESLRGGQMPRFIDGILLDDIVDTAMPG
DRVIVVGILRVIQEKREKVPTFKKVIEVNHIEPISKELEELEISPEDEGKIRELARRK
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CVDYDTEVLLGDGRKRKIGEIVEEAIKKAEKEGKLGRVDDGFYAPINLELYALDVRTL
KVRKYKADIAMKRTTPEKMLRIRTKRGREIRVTPTHPFFTLEEGRIKTKKAYELKVGE
KIATPREEAPEAEIFWDEVVEIEEYKPNNSWYDLQVPEHHNFIANGIFVHNSQLLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAA29695.1"
/db_xref="GI:3257012"
/translation="MEREBILERFLKFFREYAEGGEEPLYMGKIKDLLTITPKRSIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VANLAPRAIYTSGKSSSAAGLCVAPDTLINTDNGRVEIGKFVEEWMKEVGEISEEGIS
YAPCFRKVETFKDGKIVESPIRRVWKLRAPKKLVRIKTENGRSIALTRETKLLTINDG
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TGGWULEAGALVLADGGYALIDELDKMSDRDRSVIHEALEQOTISLSRAGITATLANR
TTVIAAANPKHGRENRRKKRSEQIDL.PPTLLSRFDLIFVLMDEPDEKVDSETARHILK
VRRGESEVYTPRIPHELLRKYIAYARNIHVYISEBAMEEIBKYYKKRRSAKKSSGD
BVTILEVGQSARKLSKVERILDIVEKLERTSERGAKIDDILEBAARFGIEKSBADDE
EKLLERGGOIYMPENGYYKTV"
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TNLLESTSSWTFLLEHCSHFFTATKPS"
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IYEPRHLPSSQALWPILYSEHLEVHEFALLHIKLDVFTSALLAFLYCNKALIGLLRHN
                                                                                                                                                                                                                                                                                                                                                                               /product-"1108aa long hypothetical cell division control
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/product="120aa long hypothetical protein"
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/protein_id="BAA29697.1"
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/protein_id="BAA29698.1"
                                                      complement(1110. .4436)
                                                                                                                             complement(1110. .4436)
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/db_xref="G1:3257013"
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Yamamoto,S., Sekine,M., Baba,S., Kosugi,H., Hosoyama,A., Nagai,Y.,
Sakai,M., Ogura,K., Otuka,R., Nakazawa,H., Takamiya,M., Ohtuku,Y.,
Punahashi,T., Tanaaka,T., Kudoh,Y., Yamazaki,J., Kushida,N.,
Masuchi,Y., Shizuya,H. and Kikuchi,H.
Complete sequence and gene organization of the genome of a
DNA Res. 5 (2), 55-76 (1998)
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on Jul 28, 1998 this sequence version replaced gi:3130861 gi:3130862 gi:3130862 gi:3130869 gi:3130869 gi:3130869 gi:3130861 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi:3131081 gi
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Horikoshi, K. is at the Japan Marine Science and Technology Center, Yokosuka, Kanagawa 237-0061, Japan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shizuya, H. is at the California Institute of Technology, Pasadena,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The other authors are at the National Institute of Technology and Evaluation, 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan. All the sequence with length 100 codons or more between ATG or GTG and stop codon are defined as CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yokosuka, Kanagawa 237-006i, Japan.
Masuchi, Y. is at the University of Tokyo, Meguro, Tokyo 153-0041,
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EYVICPVCGSPDTKIIKRDRFYFLKCEACGAETPIQHL"
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/transl_table=11
/product="140aa long hypothetical translation initiation
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                                                                                                                                        Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
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Direct Submission
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/map="544001-777000 nt. position"
complement(645. .1067)
                                                                      Pyrococcus horikoshii (strain:OT3) DNA.
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Location/Qualifiers
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BVIKSLKGKYDFILIOCPAGLQLDAMSAMLSGBEAILVTNPEISCLTDTMKVGMVLKK
AGLAILGFILNRYGRSERDIPPEAAQDVMDVPLLAVIPEDPVIREGTLEGIPAVKYKP
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/db_xref="GI:3257018"
/translation="MTRIISIVSGKGGTGKTTVTANLSVALGEMGRKVLAVDGDLTMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELPYKPDIDVREFVTVEEIMKEGYGPNGAIVESYDRIMMKFDYTLKEILELESKRUYY
LIDTPGOMETFLFHEGVKLJMENLPYPLVVYLSDPETLRKPTDYCFVRFFALLIDLRL
GATTVPALNKVDLLKEEGLEKHRKYFEDLDYLMGRLKFDPSMGGLMAYKMCSIMMEVL
PPIRVLYLSAKTREGFEDLETLAYEHYCTCGDLT"
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Iideadkvigeidkvleeerknapisaipenlyeraffyiyylekyigkggenidvi
Htkltkrikkikkykmlkdirfkkileavrlrpnsmetlsrlapgerriylgisrirn
                                                                                                                                                                                                                                                                                                                                                                             /note="similar to Swiss_Prot:P46577 percent identity:30.736 in 238aa. motif=ATP/GTP-binding site motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="245aa long hypothetical cell division inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228332 AACCGGTGAACTTCAGGAAAGAAAGAAGTATCCAGCTATTCTAGAGATCCAGGTGGTC 228391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228392 CTAMAACCGCTTACGGTTACGCTTTTATGCACGAGTTCCACGTTTTAACCTCTAAAGGCT 228451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228212 ATGGAAAGGAGAAGAAGGTTACCGACTTTAACAAATGGATAAAGGGTTACACCCTTTCAA 228271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228272 AACCIGAACACTITAAGGTTAAAGCAAGTGACGGGTTGAAATAGATGCCTGGGTAATGA 228331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to PIR:C64368 percent identity: 41.379 in 233a; PIR:B64321 percent identity: 35.841 in 227aa; owl:S76970 percent identity: 34.188 in 239aa. motif=ATP/GTP_binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1259 ggcctgcacaaatggaaggtgagacaacatatccacttattcttaacatacacggcggtc 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1319 cgcatatgatgtacggacatacatattttcatgagtttcaggtgctggcggagaggt 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1199 tacctgaagagattcaatatgctacagaagacggcgtgatggtgaacggctggtgatga 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1139 aggaagagaaacagctgactggcgcgaatgacaagtttgtcagggagcatacgatatcaa 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
                                                   /note="motif=DEAD and DEAH box families ATP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 233000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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/db_xref="G1:3257017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 368; Indels
                                                                                                                             /product="165aa long hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 227.2; DB 2
Pred, No. 2.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESKGAQAFIKLAEEVDKLAGIKAKIMY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5768. .6505)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5768. .6505)
                                                                                                                                                                                                                                                                                                complement(4979. .5737)
                                                                                                                                                                                                                                                                                                                                          complement(4979. .5737)
                complement(4439. .4936)
                                                                                                                                                                                            /db_xref-"GI:3257016
                                                                                 helicases signatures
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                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="PH0612"
                                                                                                                                                                                                                                                                                                                                                                 /gene="PH0611"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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55.4%;
                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                            /gene="PH0611
                                                                                                                                                                                                                                                                                                                                                                                                                                       A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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2 (bases 1 to 10256)
White, O., Eisen, J.A., Heidelberg, J.F., Hickey, E.K., Peterson, J.D., Dodson, R.J., Haft, D.H., Gwinn, M.L., Nelson, W.C., Richardson, D.L., Dodson, R.J., Haft, D.H., Gwinn, M.L., Nelson, W.C., Richardson, D.L., Vamathevan, J.J., Lam, P., McDonald, L., Utterback, T., Zalewski, C., Makarova, K.S., Aravind, L., Daly, M.J., Minton, K.W., Fleischmann, R.D., Ketchum, K.A., Nelson, K.E., Salzberg, S., Smith, H.O., Venter, J.C. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
Tobaco 10256)
White, O., Eisen, J.A., Heidelberg, J.F., Hickey, E.K., Peterson, J.D.,
Moffat, K.S., Qin, H., Gwinn, M.L., Nelson, W.C., Richardson, D.L.,
Moffat, K.S., Qin, H., Jiang, L., Pamphile, W., Crosby, M., Shen, M.,
Wamathevan, J.J., Lan, P., McDonald, L., Utterback, T., Zalewski, C.,
Makarova, K.S., Aravind, L., Daly, M.J., Fraser, C.M. et, al.
Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-NOV-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 228929 GAGTIGAATIGGCAATATICCCAGGAGAAAATCAIGACCIAAGTAGAICTGGGAAGCCAA 228988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 228809 CATTAAAGTACGCTCCCCAACGTTGAAACTCCCCTGCTTATAATCCACTCTACGAAGACT 228868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 228869 ACAGGTGTTGCGGAGGCATTGCAACTCTTCATATCCCTAAAATACCTGGGGAAGA 228928
                                                                                                                                                                                                                                                                                                                                                                                   Db 228689 AGAGATCAAATTGGATAAGCTTCTTCGGACAACGGATATGGTTATTACTTTG 228748
                                                                                                                                                                                                                                                       Db 228629 GTGGCTTCATGACGAACTGGATAGTCGGACATACCAACAGGTTCAAAGCCGCTGTAACCC 228688
Db 228511 -- ATAAGGGGACACTATGGGGAGAGGGATTACCAGGATTAATGGAGGTAGTGAAG 228568
                                                                                                                                            Db 228569 CATTAAGGAGATTGACTTCATAGATGGGGAAAGGCTAGGAGTTACCGGGGGTTCCTATG 228628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1859 aaaccaagcttgtccgttttccgaatgcatcgcacaatttatcacgcaccggacacccaa 1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1679 cagactggcagcttgagcatgacatgtttgaggacacagaaaagctctgggaccggtctc 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1619 agogotogatatoaaattggatoagotttoacggogtoagtgatatoggotatttottta 1678
                                                                                                                                                                                                              1499 ctatcaaacgagatccgcatattgatcctaagcggctcggtgtcacggggaagctacg 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE001879 10256 bp DNA BCT 22-NOV-1999
Deinococcus radiodurans R1 section 16 of 229 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 228749 CICCAGAICAAATAGGAAAAGAICCCTGGAGCAACTTGGAAGGTTAITGGGAAAAGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1919 gacagcggatcaagcgcctgaattatatcagctcatggttgatcaacatct 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Deinococcus radiodurans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 286 (5444), 1571-1577 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:473801 percent identity: 56.86; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mtrafialganlgDpQaTlrraltElgalgEvrgvSaLyrtapv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNLEGVHPLRLGLCWCEMEOTSRSSSOOVTDTEVASALLDTRSR
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HAAWSAGWNFTRPOAPAVLDLLGELSLDFEQAKALQRDLLQLLAQYRRKPGGQPHLIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="2-amino-4-hydroxy-6-
hydroxymethyldihydropteridine pyrophosphokinase"
/protein_id="AAF09758.1"
/db_xref="01:6457838".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:D26562 SP:P26281 GB:L06495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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/db_xref="G1:645837"
                                                                                                                                                                                                                                                                /product="dihydropteroate synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(6362. .7054)
/gene="DR0171"
complement(6362. .7054)
                                                                                                                                                                                                                                          /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="DR0170"
5893, AAAA
                                                                                   4646. .5515
/gene="DR0168"
                                                  /gene="DR0168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMVQALRVEAALA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5540. .5896
/gene="DR0169"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5540. .5896
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                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="DR0171"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="DR0172"
7034. .7849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7034. .7849
/gene="DR0172"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLCWPELGSGE"
                           gene
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                                                                                                                                                                                                                                                                                                                                                       /Cranslation-"MRLPLTVLLPLSAVLIASCGGTPSPVAATVFPATPAAQPTRTLA
AQATPPLRLPPAGKLAWDWOIGAATEAKVALPAGVSLLDLDGFETSAAKVADLKAGGY
YTVCYLNVGSYESYRPDAAQYPDSLKIQTDPRWPDESFYDIRDVFREGGVLAGILLDRR
LALCAAKGFDAVEPDNLQNDONVTSGVISRQDQLDFROWLABRAHGLAILGKNGFD
YVLQADRGGRLMVDLFDGVLNESCQRYKECGPLTEYVRGKLALNVEYRQDLNCATW
NSLGVNALFKDLSLVGKLQKAYKRVSCTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BHAHLY LIENGGHRRLDTGHDHPVCDAVGGDCHVGAFPEGPRWLDGDTLLFSSTVRGS
VGLFTAHIGGGVKAYDHDPQGYISAFTANEHGVALIRESATRPFEVELNGGRYTDLHA
RPFPVREBORYTFETELGEGSGWVLLDFGEGKVPALLNIHGGPHTDYGHGFTHEFQL
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RADALKLWDLSPLQYYENVKTPTLIYHSVLDHRCPVEQAEGWYAALHKHQVPVRFVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MNNSETPAPGPDSLIALAFPSDPQVSPDGKQVAFVLAQISEEDP
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PVYRANGADWLPERPAALWLYDVEADKLREWYAPEIGIGALGWWPDSRGVLIYOVEDE
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/protein_id="AAF09753.1"
/db_xref="G1:6457833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WOASQWRQDVYDLPLPTADAPAPQKLLDWNSAAHGLAPHPDGQRFALIGRPAGKGNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to SP:P31787 PID:1323021 PID:1620454
PID:170970 percent identity: 66.09; identified by sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INSAARPERORFTLAHEIGHAILLGDDDLISDIHDAYEGERLEGVIETLCNVAAAAIL
MPEPVIAEMLERFGPTGRALAELAKRAEVSASSALYALTEGTPVPVIYAVCAPGKPPR
EQAASDEDAGPSTEKYLTYRASSSTRGVKYTLASGTPVPADHPAALALATGMEVREES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="acyl-peptide hydrolase, putative"
/protein_id="AAF09754.1"
/db_xref="G1:6457834"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="acyl-coA-binding protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1079. .3046)
                      /db_xref="taxon:1299"
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                                                                                                                                                                                                                                                             /transl_table=11
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                                               /chromosome="1"
                                                                                                    /gene="DR0164"
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                                                                                                                                                                                                                                  /codon_start=1
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3098, .3352
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/gene="DR0166"
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                                                                                                                                                  Aeropyrum pernix (strain:K1) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /anticodon=(pos:988.
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                                                               251700 bp
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                                                                                                                                                                          ORGANISM
                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                              REFERENCE
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                                                                                                    ACCESSION
                                                  AP000062
                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                          VERSION
                                                                                                                                                           SOURCE
                                                                      COCUS
                                                                                                                                                                                                                                                                                                                                                     /note="similar to SP:P02410 PID:42855 PID:606170 GB:U00096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1806 cccgatcgagcaggcagcagctgtttatcgctctgaaaaaatgggcaaggaaaccaa 1865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1247 CCCTGTCGAGCAAGCCGAGCAGTGGTACGCCGCGCTGCACAAGCATCAGGTGCCGGTGCG 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1866 gcttgtccgttttccgaatgcatcgcacaatttatcacgcaccggacacccaagacagcg 1925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1367 GGGGCTGGACTTCTCGCGCCGGGCGGACGCGCTGAAGCTCTGGGACCTTTCGCCACTGCA 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1746 atacgcagcaaacgtggagacaccgcttttgatactgcatggcgagcgggatgaccgatg 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1427 CAACCIGATITCGTICGGGGGCACGICCGACATCGGGCIGCGCTICTGGGACGACGAGGT 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1607 crgcgccaccgrgcaccccgaccaccrgcrcaaccrrcrrcacccccrccrcrcaacccgr 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1547 GCCGCGCTGGACGCCGCAAAAACCGCCGTCATGGGCGGCGGCGACTACGGCGGCGTTCATGAC 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1727 cggccacgcrttacccacgagtrccacrtgargccgcgcgcgcgcgcrtacggcgrgrr 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1392 tatcaatccgagagaagccacggctacgggcaggaatttgtgaatgcggtcagaggaga 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1667 CTCCAACCGGGGGGTGGTGGTGGGTGGAGCGCATCTACGGGCG 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1452 ttatgggggaaaggattatgacgatgtgatgcaggctgtggatgaggctatcaaacgaga 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1512 tecgeatattgateetaageggeteggtgteaegggeggaagetaeggaggttttatgae 1571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1787 GGAAGGTGAGCAGAAAGTGCCCGCGCTGCTCAATATTCACGGCGGGCCGCACACCGACTA 1728
                                                                                                                                           TGRLGGIVPSPHIHRKSMRQVRQLAQLRPLIYLPSHDPDSLRRLQRNQPFSLT"
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity 55.7%; Score 191.2; DB 1; Length. Similarity 55.7%; Pred. No. 2.6e-48; 39; Conservative 0; Mismatches 303; Indels
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                                                                                                                                                                 complement(7904. .8999)
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                                                                                                                                                                                                                                                                                                          /gene="DR0174"
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G06-8502, Japan
The other authors are at the National Institute of Technology and The other authors are at the National Institute of Technology and Evaluation, 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan.
Evaluation, 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan.
All the sequence with length 100 codons or more between ATG or GTG and stop codon are defined as CDS mith-Waterman algorithm against Homology analysis is performed by Smith-Waterman algorithm against Homology analysis is performed by Smith-Waterman algorithm against release 36.0; PRR-Protein release 50.0; Swissprot release 36.0; PRR-Protein release 57.0; and own release 31.0; PRR-Protein release 36.0; PRR-Protein rel
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VEDAGFRVLVDTGCEPWERGLVDVDVVVFTHFHPDHIRGFHRLRAGRVAAPEGEEBPYA
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Direct Submission
Submitted (14-DEC-1998) to the DDBJ/EMBL/GenBank databases. Yutaka
Rawarabayasi, National Institute of Technology and Evaluation,
Biotechnology Center; Nishihara 2-49-10, Shibuya-ku, Tokyo
151-0066, Japan (E-mail:Kyutaka@kazusa.or.jp, Tel:+81-3-3481-8951,
Fax:+81-3-3481-8424)
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Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
06-APR-2000
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                                                                                 Aeropyrum pernix genomic DNA, section 5/7.
AP000062 BA000002
AP000062.1 GI:5105244
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                                                                                                                                                                                                                                                                                                  /translation="MOKEPPGOLEOGYGLEVPPSGVGLNADPPEAEVLPRPEILPRLRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MRYERAPDVCRAAEVLVDALGLDYIDVSRVYCVRSWGSRGRAYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="similar to OWL:SOU61050 percent identity:41.667 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MOGSRYSWPGRAARPGYAGGLGSWPFSPWPGPRPCWELFLRASI
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RVEILRDNLYNVAGVIAEGRSPSPRRPVDPRISPPPFPPABHAVHPGDVDIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="motif=neutral zinc metallopeptidases, zinc-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MEKEDGYLRIRTTPPKGCEDI.PDVHAYLGSLGVRETALGYTRV
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KGDAGEPGVVAREGREAGLRWGLGKLAILAMAGAAALLGAILEGLHPRLRGGCP"
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                                                                                            complement(1196. .1684)
                                                                                                                                         complement(1196. 1684)
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complement(2599. .3063)
/gene="APE1562"
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/gene="APE1563"
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/gene="APE1564"
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                                                                                                                     /gene="APE1560"
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2536, 2952
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/note="similar to PIR:H70375 percent identity:45.455 in

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ARILARASRMGLTVYTTPSYRAEIERFWLGNGYHPTTIARLMAWYRVKPPTTHELRLP
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                                                                                                                                                   /translation="MAGVGGRPPPSVGSVVVADTTWFTDAKLREVLGARSLBEAARIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FREGEQIVWGYPSIKRALLPRYAPPWFPGFTVLVBEKMNGYNVRVFTLGGMVYAAT
RGGILCPYTTRELRRIYGGALQKILEDLGAEGSFIAGEVVGLENPYTRYYEBAPGFG
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GVARGVDGVRVAFRKPRKSEGEIARILETGISPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MDPGSVDLEALSTRRSVRVSRFEDVVYVGFRRQFRGVPEGTLVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 172607 CAATGCTAGCTCTCAGGCTTTGCGGTGATTTACTCGAACCCCAGGGGGAGTGACGT 172666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     motif=aminoacyl-transfer RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="motif=prokaryotic membrane lipoprotein lipid
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110aa. motif=C-5 cytosine-specific DNA methylases
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                                                                                      /product="217aa long hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                           /product="138aa long hypothetical protein"
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synthetases class-II signatures"
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Pred. No. 1.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAA80565.1
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/gene="APE1567"
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/3955. /AAA
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Best Local Similarity 54.5%
Matches 369; Conservative
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Submitted (06-JUL-1999) Genoscope - Centre National de Sequencage :
Submitted (06-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
1. 304290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173144 AACCICICCGAAGCGGAACTCCTAAGAGGGGGGGGGGAAGGCITAGGGGGATAGCCTCC 173203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173084 ACCGCTCTAAAGCTGAAGGGTGTGGAGACCAGGCTTCTAGTGTTTCCAGGTGAGAACCAT 173143
                                                                                                                                                                                                                                                                                                                                                                                                                  172964 CICGAGAAATACGIIGACIIIAGCCCGCICIICTCTGTIGAGAATATIGAGACACCACIG 173023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DH 173024 CITATAATACACTCCACAGAGGACTTTAGATGCCCCCTCAGCGGTGCTATTCAACTCTTC 173083
                                                                                                                                                                                                                                                                                                                                     172904 AGCGACATAGGATGGTATTTCGCCCCGGAACTTATCTCCGCGCAAGAACCATGGAGAGG 172963
                                                                                                                                                              DB 172784 GGTGTAACGGGGGGGGGGGCTACATGACCAAGGTTATAGTAACCAAAACTAGA 172843
                                                                                                                                                                                                                                             DM 172844 AGGITCAAGGCGGCCGTCACACAGAGGAGCTGCAACAACTGGATAAGCITCTAIGGCGAG 172903
                 172667 IACAGCGAGGAGTTCGCCGAT---CTAAGGGGTAGATACGGTGTTGACGATTACTCTGAG 172723
                                                                                              172724 CTTATGAAGGTTGTTGACGAGGCCCTCTGGACTTCCCACAGCTTGACCCGCAGAGGGGT 172783
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protein (hypF)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1774 ttgatactgcatggcggagcgggatgaccgatgcccgatcgagcaggcggagcagctgtt 1833
                                                                                                                                                                                                                                                                                              1657 agigatatog---gctatttctttacagactggcagcttgagcatgacatgtttgaggac 1713
                                                                                                                                                                                                                 1597 cgctttaaagctgccgttacccagcgctcgatatcaaattggatcagctttcacggcgtc 1656
                                                       1477 gigatgcaggcigtggatgaggctatcaaacgagatccgcatattgatcctaagcggctc 1536
                                                                                                                                      ggtgtcacggggggaagctacggaggttttatgaccaactggatcgtcggggcagacgaac 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrococcus abyss1 complete genome; segment 5/6. AJ248287 AL096836 AJ248287.1 GI:5458657 complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pyrococcus abyssi"
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2 (bases 1 to 304290)
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Pyrococcus abyssi
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COMPLEMENT,3594. 3821)
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                                                                                                                                                                                                                          SYRRPIVALRKREPFPLPENLAPGLHTIGVMLPYAGTHYILEHWSKTPVYVWTSANFP
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                                                                                                                                                                                             IKGIGGIHLACDATREDVVAELRKRLFRPQKPFAIMAKDLETVKGFAYISREEEEELT
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MTASLWVAKIORPSGFWKWAVLIPALFLWVIVTSALIWFLIYVGKSSIWVSLITIVGL
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Complement(5709. .6227)
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/protein_id="CAB50157.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 158; DB 2;
                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:Q9UZA3"
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0; Mismatches
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/db_xref="G1:5458669"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATENT: WO 0065062-A 816 02-NOV-2000;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (FR) ; IFREMER
INSTITUT FRANCAIS DE RECHERCHE POUR L'EXPLOITATI; ON DE LA MER (FR)
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                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
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/db_xref="taxon:29292"
/note="Original length of seq 1: 1765118
                                                                                                                                                                                        AX041921 349980 bp DNA Sequence 816 from Patent WO0065062.
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F. is at the Center of Marine Biotechnology, University of
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Maryland, Baltimore, MD, USA.

Horikoshi, K. is at the Japan Marine Science and Technology Center, Horikoshi, K. is at the Japan.

Yokosuka, Kanagawa 237-0061, Japan.

Masuchi, Y. is at the University of Tokyo, Meguro, Tokyo 153-0041, Masuchi, Y. is at the University of Tokyo, Meguro, Pasadena,
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Shizuya, H. is at the California Institute of Technology, Pasadena.
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                                                                     on Jul 29, 1998 this, sequence version replaced g1:3130553 g1:3130577 g1:3130627 g1:3130656 g1:3130685 g1:3130676 g1:3130737 g1:3130785 g1:3130824 g1:3130828 g1:3130785 g1:3130785 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 g1:3130828 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                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 204635 AGAGGAACGAGGAACTTCAGGAAGCTAAGTCCGCTGTTCTACGCTAAGAACGTGAAGGCTCC 244576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 204575 CCTGTTGCTAATCCACAGCCTTGAAGATTATCGCTGCTCGTTGGATCAGAGCTTGATGTT 204516
                                                                                                                                                                            Db 204692 CGCGTTCTCCGACATAGGATTGTGGTT---CGACAAGGAAGTTATAGGTGAGAAACCCGCT 2Q4636
Db 204752 GAGGGACCTATTCAAGGCCGGAATCAGCGAGAACGGAATAAGCTACTGGCTAACGAGTTA 244693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1770 gettitgatactgcatggcgagcgggatgaccgatgcccgatcgagcaggcggagcagct 1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1830 gittatogototgaaaaaaatgggcaaggaaaccaagettgiocgittioogaatgcaic 1809
                                                                                                                                                                                                                                                                                                                             1710 ggacacagaaaagctetgggaceggtetectttaaaatacgeagcaaacgtggagacace 1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A-000002 AB009475 AB009476 AB009477 AB009478 AB009479 AB009480 AB0009481 AB009481 AB009483 AB009484 BA000001 , AP000002.1 GI:3236129
                                                                                                             1650 eggegteagtgatateggetatttetttacagaetggeagettgageatgaettga 17^{1}_{10}9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2000
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Pyrococcus horikoshii
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 257000)
Tanaka,T., Kawarabayasi,Y. and Kikuchi,H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 204395 GGAGTTCTTCGAGGGAAGCTC 204374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1950 ctcatggtttgatcaacatctc 1971
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First other authors are at the National Institute of Technology and Bvaluation, 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan. All the Sequence With length 100 codons or more between ATG or GTG and stop codon are defined as CDS.

Homology analysis is performed by Smith-Waterman algorithm against GenBank and GenPept release 103; EMBL release 52.0; SwissProt Erelease 34.0; pIR-Protein release 54.0; and OWL release 29.5.

Restriction map, ORF organization, Sequence alignment and more information are available at W.W. site of Biotechnology Center, URL: http://www.bio.nite.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="433aa long hypothetical
phosphoribosylglycinamide formyl transferase"
/protein_id="BAA29392.1"
/db_xref="GI:3256709"
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VVAVDRYANAPAMQVAHRSYVGNMMMINGDELWSVVEREKPDAIIPETEAINLDALFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDENGEIVTTFPKPVCHYQIDGDYHASWQPABISEKAEREVYRIAKRITDVLGGLGIF
GVEMFVKGDKVWANEVSPRPHDTGMYLASHPPGFSEFALHHRAVIGLPIPGEWVDGY
RLFPMLIPAATHVIKAKVSGYSPRFWGLVKALSVPNATVRLFGKPEAYVGRRLGIALA
WDKDVEVAKRRAEMVAHMIELRTRSSDWHDQNYEKRKHLLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDGYFVVPNARATWIAMHRERLRETLVKEAKVPTSRYMYATTLDELYEACEKIGYPCH
TKAIMSSSGKGSYFVKGPEDIPKAWEEAKTKARGSAEKIIVEEHIDFDVEVTELAVRH
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VAWITDLFTGLIEFIKGCSVHIPGSRNLCFLHKGFPKPLPVHSYPGSSCIWNYKITIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAHRTPERAYEYAKKAEERGIEVIIAGAGGAAHLPGIIASLTVLPVIGVPIKSKALNG
LDSLLSIVQMPSGIPVATVAIDNAKNAALLALRILGIKYPEIKEKLRRYMKDMKRKVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to owl:SSOUREK percent identity: 68.000 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to PIR:E64485 percent identity: 55.181
403as: PIR:S74842 percent identity: 49.869 in 397aa;
Swiss_Prot:P33221 percent identity: 50.773 in 404aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150aa; PIR:S76001 percent identity: 60.694 in 173aa; owl:BAPURKEI percent identity: 62.329 in 146aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphoribosylaminoimidazole carboxylase catalytic
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                                                                                                                                                                                                                                                                                                                                                                                                                     /map="287001-544000 nt. position"
                                                                                                                                                                                                                                                                                                                                              /organism="Pyrococcus horikoshii"
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                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:53953"
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/gene="PH0321"
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                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .257000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="PH0318"
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/gene="PH0318"
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                                                                                                                                                                                                                                                                                                                                                                            /strain="OT3"
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LKSDNIJVGMESISYPLOLIIRILSRRGVDVIKYLENHRLAIVDTFGSFHGIKATMPGV
WYLEGMLSSFTLPIKYAKAVEDHKKVWMDLNLFEGRELYGFAISMSGYLEVFFPEFTL
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                                                                                                                                     /translation="MISWEIEELDREIGKIKKHSLILIHEEDASSRCKDILFYILSRK
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DDVVFVSKIKEWAIKTLKTTNIANFWFFTYLSSGICKLFSNPLLTYKLIWALREEILK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGIIEELVSSIPEGGILAIIQKELESEGDRFGLLVLKHLLENEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLKDNEEAKEYAEHIIRKDGKVLIEERTDGVEFTLQVFTDGKKVIPMPLVOOYPHAYE
GDVGPITGGMGSYSCSNHLLPFTTEGDFERALKTLEFTIEARKEGYPYGILYGQFM
LSGEGFVLIEYNARFGDPEAINVLAVLDDNLLEIAKGIVSGSRRAKELNKATVVKYI
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ERIAENGVSYVKGPIFYRKDVGTRESVEKRIEIMKKLGKEFEPNLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mkVllvdgggrehalgealvkggaelyvvsnhrnpglmrlakdy
Glaketnvedylkfarkwglelafigpeaplergivnaleeggipavgptrearlet
nkawarefmernnipgrkmfrifddvgemrkwideygkpvvvkplgltggkgykvvgy
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PULVVAQRGRHRTYAKYFKLRKTKDNLTKGFIDEVIILDKFAQIIEIQBELIKRNVIF
IPNRSFVVYTGIDKVENBFKVPMFGTRSLLRTEERREEKSYVMLLEKAGLPYPEEVKP
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CGHASATLRESLLEKVFDMAEKYVEATKKYYPPGIIGPFTLQTVVDKDLNFYIFDVAP
RTGGGTNIHMSMGHPYGNSLWRSPMSTGRRIALEIKRGIELDELEKLVT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to PIR:A64417 percent identity: 55.478 in 442aa; owl:HUMRPS4 percent identity: 33.738 in 424aa; Swiss_Prot:P12039 percent identity: 33.819 in 352aa.motif=prokaryotic membrane lipoprotein lipid attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to PIR:H64316 percent identity: 44.847 in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAA29397.1"
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phosphoribosylamide--glycine liga
                                                                                                                                                                                                                                                                                       complement(4039. .4698)
                                                                                                                                                                                                                                                                                                                                            complement(4039. .4698)
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/db_xref="G1:3256713"
                                  /transl_table=11
/codon_start=1
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                                                                                                                                                                                                                                                                                                                      /gene="PH0322"
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/gene="PH0324"
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/gene="PH0325"
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/gene="PH0325"
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1612 ATACTCCTARTCCACTCGCTTGAGGACTACGCTGTCCGCTCGACCAGGAGCCTTATGTTC 1671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1732 cacegecacagegreegegaagecegaegeacacagecegaagegeracagecretreara 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1651 ggcgtcagtgatatcggctatttctttacagactggcagcttgagcatgacatgtttgag 1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1555 AAC---GAGAACTTCAGGAAGCTCAGCCGGTGTTCTACGCTCAGAACGTGAAGGCGCCG 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1531 cggctcggtgtcacgggcggaagctacggaggttttatgaccaactggatcgtcgggcag 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1591 acgaaccgctttaaagctgccgttacccagcgctcgatatcaaattggatcagctttcac 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1495 GCCTTCTCGGACATAGGGCTCTGGTACGACGTCGAGGTCATCGGGCCAAATCCGTTAGAG 1554
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                                                                                                                                                                                                                                                                                                                                                                                                       1135 ccGGTGATAGTCTTCGTCCACGGGGCGGAAGGGCATGTACGGACACGCCTTCGTCTAC 1194
                                                                                                                                                                                                                                                                                                                                   3; Gaps
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                                                                                                                                                 Patent: US 5985646-A 1 16-NOV-1999;
                                                                                    (bases 1 to 1869)
Murphy, D., Reid, J. and Robertson, D.
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ILFKVSPEKAKEELYEKLVEGGLPEETAREVSEKLLEKEEALIKLLVPEEEBNEFRAA
LYTGIAYLFGVAFPVTPYFFASTSLRALPISVTLAGLALIVATSISLISGISIRKKV
IEMYTGLGAAFLSVIFGHIMESLFNVSAL"
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                                                  EAKHAKFWHDFLVRRGVKPKKPRIKKLTFFTVKLLRKLFGPAMVVSMLEMGENSAIOK
YFKFFGEFSDEITEEEFFGLRGIIIDELEHEKFFSESKKLFHVENIRDFYLGMNOGLV
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                /db_xref="GI:3256716"
/translation="MSSAIKIAEEFYNDEYSDSVLYABLAKYEKNKEIKEEFLRLSRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247476 CITTAAAGCTGGAATAAGCGAGAACGGAATAAGCTACTGGTTAACAAGTTACGCCTTCTC 247535
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                                                                                                                                                                                                                                                                                                                                                                                                       247176 AGTCTTCGTCCACGGTGGGCCAAAGGGAATGTACGTTAAGTACGAGATGCA 247235
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                                                                                                                                                                                                                                                                                                                                                                         1299 tettaacatacaeggeggteegcatatgatgtaeggacatacatattteatgagttea 1358
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                                                                                                                                                                                                                                                                                                1239 ggtgaacggctggctgatgaggcctgcacaaatggaaggtgagacaacatatccacttat 1298
                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                        Score 150.6; DB 2; Length 257000;
Pred. No. 3.9e-35;
0; Mismatches 344; Indels 6;
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Best Local Similarity 52.3%;
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247833 TGAGAGGAAGCTC 247845
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1135 CCGGTGATAGTCTTCGTCCACGGGGGCCGAAGGGCATGTACGGACACCGCTTCGTCTAC 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1771 cttttgatactgcatggcgagcgggatgaccgatgccggatcgagcaggcggagcagctg 1830
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                                                                                                                                                                                                                                7.6%; Score 149.8; DB 9; Length 1869; 52.3%; Pred. No. 2e-35;
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0; Mismatches 322; Indels
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Kawashima'T., Yamamoto,Y., Aramaki,H., Nunoshiba,T., Kawamoto,T.,
Watanabe,K., Yamazaki,M., Kanehori,K., Amano,N., Ohya,Y., Makino,K.,
and Suzuki,M.
  Thermoplasma volcanium genomic DNA, complete sequence, section 3/6
                                                                                                                                                                                                                                                                                 Determination of the complete genomic DNA sequence of Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                             Kawashima,T., Amano,N., Koike,H., Makino,S., Higuchi,S.,
Kawashima Ohya,Y., Watanabe,K., Yamazaki,M., Kanehori,K.,
Kawamoto,T., Nunoshiba,T., Yamamoto,Y., Aramaki,H., Makino,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 306728 AATAATAACAGATAAAATAATCCGACGATACTCTTTGTCCACGGTGGGCCTCACGCCAG 306787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaeal adaptation to higher temperatures revealed by genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-DEC-1999) Masashi Suzuki, National Institute of Bioscience and Human-Technology, Centre of Structural Biology; Higashi 1-1, Tsukuba, Ibaraki 305-0046, Japan (E-mail:namanodaibh.go.jp, URL:http://www.aist.go.jp/RIODB/archaic/, Tel:81-298-54-6582, Fax:81-298-54-6041)
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51.5%; Pred. No. 2e-29;
itive 0; Mismatches 329; Indels 15; Gaps
                                                                                                                                      Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of thermoplasma volcanium
Proc. Natl. Acad. Sci. U.S.A. 97 (26), 14257-14262 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The most recent annotation is available at http://www.aist.go.jp/RIODB/archaic/Location/Qualifiers
                                                                                             Thermoplasma volcanium (strain:GSSI) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PASE COUNT 105792 a 65548 c 68174 9 104286 t
                                                                                                                                                                                                                                                                                                                                  Jpn. Acad. 75, 213-218 (1999)
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                                                                                                                    Thermoplasma volcanium
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hes 365, Conservative
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                                                                                                                                                               Thermoplasma.
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Ng.W.V. Kennedy.S.P., Baliga.N., Thorsson.V.; Sbrogna.J.,
Shukla.H.D., Lasky,S.R., Baliga.N., Thorsson.V.; Sbrogna.J.,
Swartzell.S., Welir.D., Hall.J., Dahl,T.A., Welti,R., Goo,Y.A.,
Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,
Maddocks,D.G., Jablonski,P.E., Krebs,M.P., Angevine,C.M., Dale,H.,
Isenbarger,T.A., Pock,R.R.F., Pohlschrod,M., Spudich,J.L.,
Jung,K. H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P.,
Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ng,W.V., Kennedy,S.P., Mahairas,G.G., Berquist,B., Pan,M., Shukka,H.D., Lasky,S.R., Baliga,N., Thorsson,V., Sbrogna,J., Swartzell,S., Welr,D., Hall,J., Dahl,T.A., Welt,R., Goo,Y.A., Swartzell,S., Weller,K., Cruz,R., Danson,M.J., Hough,D.W., Leithauser,B., Keller,K., Cruz, Krebs,M.P., Angevine,C.M., Dale,H., Isenbarger,T.A., Peck,R.F., Pohlschrod,M., Spudich,J.L., Jung,K.-H., Alan,M., Fretles,T., Hou,S., Daniels,C.J., Dennis,P.P., Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and Dassarma,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE005114 9825 bp DNA BCT 12-FEB-2001
Halobacterium sp. NRC-1 section 145 of 170 of the complete genome.
                                                                                                                                                                                                                                                                                                                              pd 307262 cadargrecraradaacaggeegaacaartrracaeggerrreaagaraaacggagrega 307321
                                                                                                                                                                                                                                                                                                                                                                                                                               DU 307322 AACAAAACTIGICAGAAGTATCGGIGATICACAIGAACAIGCCCGAAAAGGAAACCAGA 307381
                                                                                                                                                                                                            307202 AAITTAFCACGTAAAGAGGTTAAAACGCCAATATTGTTTATACACGGGAGAGAACGATTC 307261
D 307082 ATCGAATTTTTGAGCATGTGCGGTACTAGCGATATAGGTTTTGGTTCAATGCCATAGA 307141
                                                                                                                         307142 AAAIGCCGITAAGGAICCIIGGAIAICIGAAAAICAAAAIIACACIGAIGAAAAIGICACC 307201
                                                                                                                                                                                                                                                                             1800 ccgatgcccgatcgagcaggcggagcagctgtttatcgctctgaaaaaaatgggcaagga 1859
                                                                                                                                                                                                                                                                                                                                                                              1860 aaccaagettgtccgttttccgaatgcatcgcacaatttatcacgcaccggacacccaag 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    From the cover: genome sequence of halobacterium species NRC-1
Proc. Natl. Acad. Sci. USA 97 (22), 12176-12181 (2000)
                                                                                                                                                                            1740 titaaaaatacgcagcaaacgtggagacaccgcttttgatactgcatggcgagcgggatga 1799
                                                                           1689 gctt-----gagcatgacatgtttgaggacacagaaaagctctgggaccggtctcc 1739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307382 GAACATGAGAAGAGGCTAGAACTCAAACTTGAATGGTTCAAATCACAT 307430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1920 acagoggatcaagogoctgaattatatcagotcatggtttgatcaacat 1968
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/transl_table=11
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SGYEIIDGAMFTEFTAFETPLTETTGERVTGLIDDVVIINVLRAATPFVEGLLKAFPRA
KQGVISAGRDEDAGMDADGEFPITVDYVKLPDISEGDTVIVADPMLATGSTMCTVLDH
VTDEMPAAGVEDLFVLSAVSAPDGLLRVGDQFFDADLLTVAIDDTLTDDGYIVPGLGD
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ERAVSKPESWIDGPAGDIQGWYLTPPEFDPEETYPLVVNVHGGPHLAWSAAGTWHF
FQTLAARGYVVEWCNPRGSTGYGGEWLRAVERDWGAVTLADVAAGVAAVTDRDYVDAD
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DADDRLEWATEAATPADSADSTVVTTVEGWGPTLAVHGSRVAYTTFADDPTLTOTAV
EVFDRDTGATDRLTDGVDRTVAERTAGHAPEWGPDGBHLYVCTPDEGGYVLRRVAADT
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RDNAFLWAQSPAAHTDAVDTPTLLVHSEADYRTPANTAELFYRLLKKHGVDTRLVRYP
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GEATRITDVIGGVSNIAWGPDGDRVAFLQAVRPAERAEELDREHDGEYERDTPDPRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRCAFVENYPGFPGGIDVPTLRGLFHDHAETAGCDLIADTVESVDRPSDDDTGFVVET
QDGRRYYTDTVLAAAAKYDGSYLRPVVGDSAFETHDHHGESRERFDDAYADAGGRTPVD
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RVRSQEEFVFEVNI NDDDLKSAVQDHLSSFEALDRWHVDTERETDVAEAAEGVDPPKQ
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STASGOGRAVIAATFGYTALVLLFGESAPKSYAVENESWALSIAFPLØWSRELYDI
VVLEDYLTRAVNOFTGGRAATESYYNTSELQDMIRYGEREGVIEEDEREMLQRIFRE
NNTIAKEVMTPRALDOLIEPTIHVEESKUVDDLLQEMODERVOLVVVIDERGTIEGT
VRESLYGETEDALDDLIEPTIHVPESKNVDDLLQEMODERVOLVVVIDERGTIEGTI
TAEDITEEIVGETLDGGEDLPTLSVDEDTVRYRGEVNIEEVNEALNIDLPEGGFFETI
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DSTGNGA"
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RYVEPMHSERDAVKRIVGARTVPAIVDDETGVAMAESANIVAYLDATYGGGE"
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               CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2552 ACCCCGATGGGTGAAGAGGTCACGCTAACGCGCGGAACCGCGACTACCTCGACGAG 2611
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                                                                                                                                                                                                                                                                                                                                          Pred. No. 4e-29;
0; Mismatches 401; Indels 15; Gaps
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                                                                                                                                                                                                                                                                                                   6.6%; Score 130.4; DB 1; Length 9825; 50.6%; Pred. No. 48-20.
/db_xref="GI:10581722"
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/gene="VNG2312C"
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Search completed: September 26, 2001, 08:23:28 Job time: 19340 sec